Page 1

Tue Jan 28 09:45:03 2003

	GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.	
M protein - pr	M protein - protein search, using sw model	
tun on:	January 28, 2003, 08:38:45 ; Search time 12.9816 Seconds (without alignments) 1811.96 1111/on cell updates/sec	
ritle: Perfect score: Sequence:	US-09-730-465-2 1356 1 WWGSDAGRALGVLSVVCLLVLYMNGILKCDRKPDRTNSN 250	
coring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

283224

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

prR_73:* 1: pirl:* 2: pir2:* !: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	form			-20
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	abrane .	N.Alternate names: CD58 antigen; surface glycoprotein LFA-3		S Stoyt
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RESULT A28564	ymphot	Alte	C; Species: Homo sapiens (man)	- Pate
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N. Accession (ASSS).

Associated (Type) man.

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A: Notecule (1905 mRNA)
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Access references; OBE-1034-00-0 (MIR-153420
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Score 1326; DB 2; Length 250; 100.08; Query Match Rest Local Similarity

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Page 2

	RESILT 3 Selia archee glycoprotein COD preductor - Norse North and archee glycoprotein COD preductor - Norse North and archee glycoprotein COD preductor - Norse Confect 13-701-1959 sequence_archee glycoprotein COD - Norse State Cod - Norse St	RESULT 4 Alto and the CAN procured - Number Hast-Li CDAS; Loukocyte antigen Huly- NATORIA and Long CAN procured - Number Hast-Li CDAS; Loukocyte antigen Huly- NATORIA - Species How a page of the CAN Procured Hast-Li CDAS; Loukocyte antigen Huly- CA Species How A 1944 - Species How A 1945 - Species How A 1944 - Species How
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Systep P. H.; Chang P. C.; Hissey, R. E.; Horsey, R. E.; Hochardson, N. E.; Spagnoll, G. Proc. Mall, Acad. Sci. U. S. N. 84, 7391-7345, 1387
Proc. Mall, Acad. Sci. U. S. N. 84, 7391-7345, 1387
Proc. Mall, Acad. Sci. U. S. N. 84, 7391-7345, 1387
A. Reference manner: S02202, WILD 6720431; PAID:285036
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C:/Comment: C:D 1sa surface antigen expressed on all peripheral blood f-cells. It app
or is closely associated with. The erythrocyte receptor.
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A:Residues: 152-1312-163 68A2>
Residues: 15-151-163 D. Oven, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton,
REBO J. 7, 167-1681, 1988
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Rissed B. Artific A. B. Artific A. Bt. 3365-1389, 1897
Proc. Mail. Acad. Sci. U.S.A. Bt. 3365-1389, 1897
A.PILES Richelus Caning of the Construction and Proceedings of the Construction of the Constr
Riscoedli, M.A., Erroom, M.H. in Dunne, J., Oosen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 8128-9722, 1966
ANTILLE NOIS-LIZ CLOTING Of the human T. Tymbhocyte surface CD2 (T11) antigen.
A Reference number: AZ6486, MADI: 87041253; PMLD:349670
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A introduce: 2014; 1280,1 2004; 2464

Colsepteding Y-cell and the elyoporoen cop

Cheapords: 91yoporolon: Y-cell introduced protein

Cheapords: 91yoporolon: Y-cell introduced protein

Pro 2014; 240yoporolon: Y-cell and the protein COD status predicted own:

Pro 2014; 240yoponin: consequence status predicted corps:

Pro 2014; 240yoponin: consequence status predicted corps:

Pro 2014; 240yoponin: introducible status predicted city.
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A. Mostadiues: 1. 267, 0′, 267, 351, SEE:
A. Crossidiues: 1. Ceft. references: G8:MIG445; NCBC; PIDN:AAA51738.1; PID:9178669
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A:Residues (1738, W., 740, 700XTHCPLFLIXXDRNCLEQ' <SAl>
A:Residues (1846, W., 740, 700XTHCPLFLIXXDRNCLEQ' SIDN:AAA51946.1; PID:g180094
A:Accession: A30430
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Fresholders, 224-65, XY, 504 c2823-
Fresholders, 224-66, XY, 504 c2824-
Fresholders, 224-66, Sci., 19. SA, 84, 7256, 1987
A. McRetenen number: 78416.
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23.0%; Pred. No. 0.032;
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A:Molecule type: 1-338, M', 340, 'QOKTHCPLPLIKKDRNCLFO'
A:Residues: 1-338, M', 340, 'QOKTHCPLPLIKKDRNCLFO'
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A;Cross-references: GDB:118735; OMIM:186990
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A; Residues: 1-351 <LAN>
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A:Molecule type: mRNA
A:Residues: 1-338, W',
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A:Tresstudes: 1.251 CAID.
A:Tress-references: GB:M19806; GB:J03622; GB:J03623; MID:9180079; PIDN:AAAS3095.1; PID:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Characterization of the Epstein-Barr virus-inducible gene encoding the human le A:Reference number: A39689; MUID:91141511; PMID:1847502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Molecule type: protein
A:Residues: 'D',30-39,'H',41-43,'S',45-53,'A',55-56,63-74,'E',76-81,'X',83,'X',85,'X',87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accessive elements of MASSIL; NID-9179494; PIDN-BAANS602.1; PID-9179495

MACCOSS TREE MASSIL; MID-9179494; PIDN-BAANS602.1; PID-9179495

MASSILE MACCO 175, MASSILE MASSILE ACCOUNTS TO THE MASSILE ACCOUNTS TO THE MASSILE MASSILE MASSILE MASSILE MASSILE MASSILE ACCOUNTS TO THE MASSILE MA
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A. McCross-reference: PMEL-NGG18 INID-29454 FIDN: CAA2367 1, PID-973724
A. McCross-reference: PMEL-NGG18 INID-29454 FIDN: CAA2367 1, PID-973724
NGI-0611, 1801-11, 181-1827, 1991.
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Cikeyordes glycoprotein; phospatidylinositol linkaeş surface antigen
Cikeyordes glycoprotein; phospatidylinositol linkaeş surface antigen
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F-tol. 42 (Domain: signes surface)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 TIXNLTSSDEDEYEMESPNIT---DTMKPFLYVLESLPSPTLTCAL----TNGSIEVQC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 YISKVQKEDNSTYIMRVLKKTGNEQEWKIKLQVLDPVPKPVIKIEKIEDMDDNCYLKLSC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 MIP-BHYNSHRGLIMXSW---DCPMBOCKRNSTSIYFKMENDLPOKIOCTLSNPLFNFFS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 VIPGESVN-----YTWYGDKRPFPKELQNSVLETTLMPHNYSRCYTCQVSNSVSSKNG 207
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                                                                                                                                                                                                                                A.Cross-references: GB:M59904; NID:q180138; PIDN:AAA62834.1; PID:q180139
                                                                                                                                                                                                                                                                                                                                                                                                                      A.Title: Molecular cloning of the lymphocyte activation marker blast-1. Keference number: A27236, WUID:88111558; PMID:2828034 A.A.CossSion: A27336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79: Indels
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A:Map position: 1q21.3-1q22
                                                                                                                                                                                                                                                                                        EMBO J. 6, 3695-3701, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-65, 'N', 67-243 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 9.3%;
1 Similarity 27.0%;
50; Conservative 3
                                                                                                  A: Molecule type: mRNA
A: Residues: 1.7W'.3-243 <VAD>
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A: Residues: 1-27 <FIS>
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                            A;Accession: A53245
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Refutiger, S.: Hophes, G.J.; Healy, M.C.; Jaton, J.C. J. Bell.; Chem. 252, 192255, 1936 A. Fille: Robbit ascretory components of different alloypes wary in their estrohydrate A. Reference number, 78877; WIDSERSEND31, PMID:31339 A. Roberson (M. P. A. M.	C Superfailly sectory Component, immunosibablish monology or (Superfailly sectory Component, immunosibablish recomposition) (Copycess slatentive splitting) objication (sycopocian), immunosibablish recomposition) (Copycess slatentive splitting) objication (sycopocian), immunosibablish sectory Component is status predicted GAMTP- 19-595/Product; free secretory component is status predicted GAMTP- 19-595/Product; free secretory component status predicted GAMTP- 19-595/Product; free secretory component status predicted GAMTP- 19-595/Producti immunosipolatin hosology CAMP- 19-595-Producti immunosipolatin hosology CAMP- 19-595-Producting immunosipolating hosology CAMP- 19-595-Producting immunosipolating hosology CAMP- 19-595-Producting immunosipolating hosology CAMP- 19-595-Produ	Juer Jest dato		Db 48 PCKTSSEX. "Y-FCEMPAGE	03139 03139 C. Specials alkina consolidate (Activities of State (Colonia) C. Decessis alkina consolidate (Activities of State (Colonia) C. Decession: 180139 sequence_crision of State (State (Colonia) C. Decession: 180139 sequence_crision of State (Colonia) Decession: 180139 sequence_crision of State (Colonia) Read 1.7% (Dec. 2007-2009) 1888 A Arviens 3.; Williams, A.P. Williams, A.P.	A TILE: THE MEN COT'S BRILDERS OF THE LEMBORYDERS AND GROUDELINE IS In a subset of the Americance manager; SOLDS: WILD: SESSION STATES OF THE AMERICAN SOLDS: WILD: WILD	Best Local Similarity 21.9%; Pred. No. 0.23; Matches 55; Conservative 43; Mismatches 99; Indels 54; Gaps 14;
DD 143 TATERWARTT—— DEPARTOGNALKAGAVTHAR—— 111 OY 180 DIPORTOCTISSHEPTINTTIPSSHIPMALEI —— PANTTITUVA 234 OY 225 MILKORDEPRINS 150 DD 235 TATERWARTT	PROUNT OF CONTROL OF C	Cidentities A Map Sellicini 1 6 (4) Score 106; DB 2; Length 490; Best Loran 1 8 (4); Score 106; DB 2; Length 490; Best Loran 2 Statistic 1 7 3, 14); Preed, No. 0, 22; Length 490; Best Loran 2 Statistic 1 7 3, 14); Preed, No. 0, 22; Length 490; Best Loran 2 Statistic 1 7 3, 14); Preed, No. 0, 22; Length 490; Best Loran 2 Statistic 1 7 3, 14); Preed, No. 0, 22; Length 490; Best Loran 2 Statistic 1 7 3, 14, 14, 14, 14, 14, 14, 14, 14, 14, 14	HPPENWPLKEVLAKKOKDKVAELENGEFF	09 134 TWGSTOOCHEPTY—VERSIGLIANGEDERIC STREET STREE	Oy 231 VLYMSTIACDMEDORYNG 249 DD 409 LAAAQMFUKISSMPTIANA 423 REGERG 7 REGERG 7	Secreboy Component presence - rabbit Configuration answer poly-13 receptor; polymeric immunositchailur seceptor Configuration answer poly-13 receptor; polymeric immunositchailur seceptor Configuration and Configuration and Co	A.Cros8-references: GB:X00412; GB:X01291; NID:91595; PIDN:CAAZ5118.1; PID:91596 A:Notes: the authors translated the codon ACC for residue 64 as Asn

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 LNDYYILAAQGICHYMLDTLLVFM-----PT---TLDYLRINKKFMSPTHV-SYGG- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 INYSWDCPMEQCKRNSTSIYFKWENDLPQKIQCTLSNP-----LFNTTSSILLTTCIP 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 DEDEYEMESPNI----TOTMKFFLYVLESLPSPTLTCALTNGSIEVQCMIPEHYNSHRGL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 NVTFHVPSNVPLKEVLMKKQKDKVAELENSEFRAFSSFKNRVYLDTVSGSLTIY-NLTSS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.4%; Score 97.5; DB 2; Length 276; 22.1%; Pred: No. 0.81; Ve. 35; Mismatches 67; Indels 57
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Matches 45; Conserve
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Aiwesludes: 11414 (2005)
Actoss-references: GB:AA010592; NID:g12580714; PIDN:CAC27032.1; GSPDB:GN00151
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C.Species: Rickettsia prowazekia prowazekii
C.Species: 21-80-1998 Rsequence_Eevision 21-Nov-1998 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 ---CKRNSTSIYFKMENDLPQKIQCTLSNPLFNTTSSI-ILTTCIPSSGHSRHRYAL-IP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 ENSEFRAFSSFKNRVYLDTVSGSLT---IYNLTSSDEDEYEMESPNITDTMKFFL---- 118
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                                                                                                                                                                                                                                                                                                                                                          65 B-LENSEFRAFSS-FKNRVYLOTVSGSLTIYNLTSSDBDEYEMESPNIT-DTMKFFLYVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 RYFPNGKKTVFESVFKDRVDLDKTNGALRIYNVSKEDRGDYYMRMLHETEDQWKITMRYY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ESLPSPTL----TCALING-SIEVQCMIPEHYNSHRGLIMYSW---DCPMEQ----- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 DLVSKPAIKIEKTKNLTDSCHLRLSCKVED----OG-VDYTWYEDSGPFPORNEGYULR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BO ITITEHNKSTEY-----TOOVSNEVSSENDILYFIEDSGROWHNTAAMIN 228
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                                                                     13 VLSVVCLLHCFGFISCFSQQIYGVVYGNVTFHVPSNVPLKEVLWKKQK------DKVA 64
                                                                                                                                                                      11 ILESLALSLYTGPQDQSVPNVNAITGSNVTLTI----LKHPLASYQRLTWLHTTNQKIL 65
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2.8%; Pred. No. 3.7
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C:Keywords: nucleomorph
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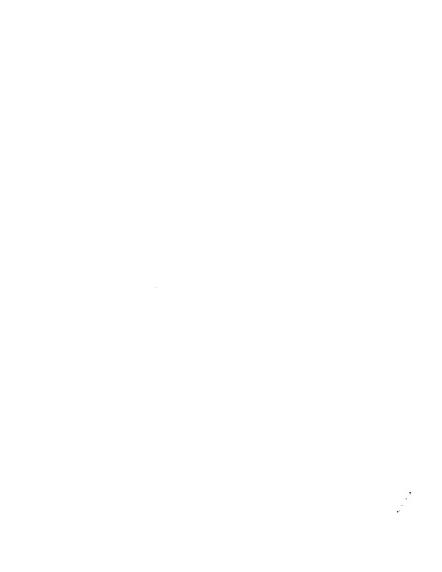
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A: Nel Geuji e type: DNA A: Residents 1-1902 (STE) A: Croces-references: BMEL: (128271) NTD:9691611 PTDN:AAG6037.1; PTD:9691669; NTFS: IPPRI A Momentaer 1968; DW. 106-313; PV. 227-439; TRV. 442-507; VV. 509-521; II. 525-577; EV. 5 PRIMORE CONTROL OF TRANSPORTED AND A MOMENTAER AND A Avencine: 12-16; WW. 169-132, VP.137-439, SBC.442-597, VV.509-537, II.525-577, EV. Avencines: 12-16; WW. 169-132, VP. 1327-439, SBC.442-597, VP. 509-537, II.525-577, EV. Avence references Board Managed States and States A.Title: Purification and crystallization of glycogen phosphorylase from Saccharomyce A. Reference number: S24010; MUID:92309401; PMID:1613787 A. Accession: S24010 A.P.T.Lia. Sequence mid minists of chromosome 2 of the plant Arebidopsis thelians. A.Rocession: Bears A.B.A.C. WHID:20083487; PMID:10617187 A.Rocession: Bears Preliationry A. MADIBLOUE TOTAL THE THE TABLE TO SERVICE THE SE J. Divegee prophortysase (E. 2.4.1.1.) - yease (Sacchardones cerevistas) RAILectera omes: GPH protein protein posts. Procisin PRRISO. C. Specius: Seculomyrope carevisiane on 'Oracles' protein PRRISO. C. Receins and PRESIDENT Seculos. Proceedings of the PRESIDENT CONTROL of the PRESIDENT SECULOR SECURISES. SECURISES. RESIDENT SECURISES. PRESIDENT SECURISES. SECURISES (SISSE): SECURISES SECURISES (SISSES). SECURISES SECURISES. SECURISE 70 EFRAFSSFKNRVYLDIVSGSLTIYNLTSSDEDEY------EMESPNITDTMK 115 259 DINLESSLKSLTYLDLSGNSISPRSLRS---DLYIPLTLEKLLLEQCGIIEFPNILKTLQ 315 116 FPLYV-----TCALTNGSIEVQCMIPEH 147 316 KLEYIDMSNNRINGKIPEWLWRLPRLRSMSLANNSPNGFEGSTDVLVNSSMEILFM---H 372 148 YNSHRGLI-------MYSWDCPMEQCKRNSTSIYFKMENDLPQKIQCTLSNP 192 373 SNNTOGALPNIPLSIKAPSAGYNNPSGEIDLSICNRSSLAALSLPVNNPTGKIPOCLSNL 432 64; Indels 69; Length 740; A:Description: The sequence of S. cerevisiae cosmid 9584. A:Reference number: S61139 A:Reference number: S61144 DB 2; 1larity 24.18; Score 93.5; Di Conservative 21; Mismatches submitted to the EMBL Data Library, August 1987 A. Meference number: \$29860 A. Accession: \$29860 193 LF----NTTSSIILTTCIPSS 209 433 TPVHLRKNNLEGSIPDTLCAGDS 455 A; Molecule type: protein A; Residues: 2-8, 'X', 10 <RAT> E, Lerch, K.; Fischer, E.H. Blochemistry 14, 2009-2014, 1975 Nature 402, 761-768, 1999 Query Match Best Local Similarity Natches 49: Conserv A; Map position: 2 RESULT 14 ę ó ò q 8 A.Cross-references: EMBL:U32445; NID:g914969; PID:g914988; GSPDB:GN00016; MIPS:YPR117w C.Genetics: Rillin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y.; N. Köb, H.; Moffet, K.S.; Croflat, L.J.; Shen, W. Yankhen, S.B.; Umayon, L.; Tallon, 1 elss, D.; Midran, W.C.; Hilte, O.; Elson, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, 13; 14; probable membrace protein (PRIJA* - yeast (Saccharcmyces cerevisiae)
NA.Ltearnte names: hypothelicial protein 192381.
C. Species: Saccharcmyces cerevisian C. Species: Saccharcmyces cerevisian C. Perez. 1996 flext_change 19-Apr-2002
C. Pate: 1-7-2ar-1996 flext_change 19-Apr-2002 2168 LOCFNOOENPVYTELLAPPYENSSYN--KNAPMVEIFWILGPSVGGISDLODLIVSLOPL 2225 2226 IFK-----SPHKTSEKLANYLFPKIEQTSIEPNSPELVPRSSTSSFF----SS 2269 2270 SPVLRHSLSNGSLSV----YDAKD---VDSWDLRSIQSKEGIKKHKGDHRKLSASLF 2319 hypothetical protein Arch2031800 [inproced] - Architologesis thaliana pergelesis Arch2006psis thaliana (ecose-ear cress) of Concess-ear Cress) Concession: 86474. Concession: 86474. 2320 VQPDYNINEMVK--RSCTPPNVKSIIIRKTLMSVCYKGS-HS----LLJDVNNLIVRVPV 2372 126 SPTLTCALTNGSIEVOCMIPBHYNSHRGLIMYSWDCPMEOCKRN-----STSIY 174 175 FKMENDLPQKIQCTLSNPLFNTTSSII----LTTCIPSSGHSRHRYALIPIPLAVITTCI 230 88 GSLTIYNLTSSDEDEYEME -- SPNITDTM -- KFFLYVLESLPSP -- -- - TLTCALT 134 83 GDLKIKNLTRDDSGTYNVTVYSTNGTRILDKALDLRILEMVSKPMIYWECSNATLTCEVL 142 Gaps 70 EFRAFSSFKNRVYLD-TVSGSLTIYNLTSSDEDEYEMBSPNI---TDTMKFFLYVLESLP 125 Gaps 26 GTWAGALGEGINLNIPNFONTDDIDEVRHERGSTLVAEFKR-KMKPF--1KSCAFFIIAN 82 135 NGSIEVOCMI---PEHVNSHEGLIM-YSWD---CPMEDCKE-NSTSIYFKME-NDEPOK 184 26 ISCPSQQ-----IYGVVYGNVTFHVPSNVPLKEVLM------KQKDKVAELENS 69 35 GVVYGNVTFHVPSNVP-----LKEVLMKKQKDKVAELENSEFRAFSSFKNRVYLDTVS 87 143 EGT-DVELKLYGGKEHLRSLROKTMSYOWTNLRAPF-KCKAVNRVSOESEMEVVNCPEK 199 34: 70; DB 2; Length 2489; 84; Indels Indels Asimatical to the EMBL Data Library, July 1995
Standited to the EMBL Data Library, July 1995
A Mediciption; The sequence of S. cerevisiae cosmid 8283.
A Medicanno number: 859764
A Medicanno number: 859764
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A Modecula trype: DAA Keywords: transmembrane protein 16-32/Domain: transmembrane *status predicted <TML> 116-35/Domain: transmembrane *status predicted <TML> :69 ; Score 95; DB 2 ; Pred. No. 22; 39; Mismatches : Pred. No. 1.7; 26; Mismatches 7.28; 27.9%; A; Cross-references: SGD: S0006321 21.28; 52; Conservative 50; Conservative Best Local Similarity Matches 50: Conserva Similarity A; Residues: 1-2489 <NEL> A; Gene: MIPS: YPR117w 2373 LKYHN 2377 C; Accession: S59782 231 VLYMN 235 Ouery Match Best Local Matches RESULT 13 ò ò 8 ô ò q g ò g

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102 EY----LUCA 132
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                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 NVPLKE-----VLWKKQKDKVAELENSEFRAFSSFKNRVYLDTVSG-SLTIYNLTSSDED 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 NISIDELARMRIYWQKDQQMVLSIISGQVEVWPEYKNRTFPDIINNLSLMILALRLSDKG 111
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                                                                                                                                                                                                                                                                                                                                   87:
                                                                                                                                          Query Match 7.0%: Score 92.5; DB 2; Length 299; DB 8ct Local Smallarity 19.4%; Pred. No. 2.4; Matches 47; Conservative 38; Mismatches 70; Tondale #
               C:Superfamily: B-lymphocyte restricted antiden B7
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C. Sajericani; Posporytein; Pyridoxil phosphate; Pyridoxil phosph
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A:Reference number: SS0938; NUID:99176711; PMID:7871892
A:Accession: SS0939
Arītie: Amino acid sequence of two functional sites in yeast glycogen phosphorylase. Arkerence mumber: 532596; MUID:75146541; PMID:1092346 Arkecession: 532596; MUID:75146541; PMID:1092346
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                                                                                                                                                                                                                       7.0%; Score 93; DB 2; Length 902;
24.6%; Pred. No. 8.8;
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A:Map position: 16R
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A; Molecule type: protein
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Feast IO, 1527-1530, 1994
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MEDILLE-9513727; Banked-1200055; P. A., Harlos K., Stuart D.I., A cones E.Y., Tavis S., Safate L.W., van der Wener A., Harlos K., Stuart D.I., A cones E.Y., Tavis S.J., vo. 109-14141 denain of COSE (1999 (1994)) or 12-14141 denain of COSE (1994) or 100-14141 denain of COSE (1994) denain of COSE
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MEDILAND-88155009; Pubmed-5910199.
Medilache S. Ferender C. Farender C. Faren
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Barder H.E., Destin H.L., Springer T.-P., Springer T.-P., Perlancy Structure of Tymphocyte function associated antigen 3 (LPA-PELLANCY TIPE LIGHT OF CONTROL OF STRUCTURE OF TAX. The Ligand of the T Tymphocyte CD2 stycoprotein.", J. Exp. Med. 166:1923-921/1997).
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ATTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; AND PRODUCED BY ALTERNATIVE SPLICING.
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15-JUN-2002 (Rel. 41, Last annotation update)
Lymphocype functions associated autigen 3 precursor (Ag3) (Antiqen CDSB) (Surface diversories in the contraction of the contraction 
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Mammalla; Butteria; Primates; Catarrhini; Mominidae; Momo.
NCBL_Taxio-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "An LFA-3 cDNA encodes a phospholipid-linked membrane protein
monicogous to trs receptor CD2.";
Nature 239:840-842(1987).
                                                        P52467
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CD58 OR LFR3.
Homo sapiens (Human).
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MEDLINE-88009714; PubMed-3309127;
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MEDLINE-88039074; PubMed=3313052;
Seed B.;
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P19256; Q96K19;
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P27573 P
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                         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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CD48_HUMAN
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CD80_MOUSE
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his assistance marty is opergright. It is produced through a collaboration between the Sates institute of injustmention and the Bedin contraction between the Sates institute of injustmention and the Bedin contraction to the Sates proposed in the Sates 
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18-807-1990 (Rel. 16. Last sequence update)
15-0W-2002 (Rel. 11. Last annotation update)
06-05-38 surface antigen procursor (Roll surface antigen) (BLAST-1)
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SERVING TO THE STANDALIGIC SET AND TH
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-- SINGLARIY: BEANGNS TO THE INMUNOCIDENTIA WERFARIY.
-- SINLIARIY: COMPAINS I IMMUNOCIDENTH-LIKE C2-TYPE DOMAIN.
-- SINLIARIY: CONTAINS I IMMUNOCIDENTH-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butherla; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                    STANDARD:
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241 DRKPDRTNSN 250
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                                                                                                                                                                                                                                                                                                                                                                                                 (CD48) (HM48-1).
CD48 OR BCM-1.
                                                                                                                                                                                                    CD48_MOUSE
P18181:
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PROPER
LIPID
                                                                                                                                                                  CD48_MOUSE
ID CD48_M
                                                                                                                                                                                                                                            while states earny marty is copyright. It is produced through a cultibraction between the Sulss institute of Historicametics and the Best own statement of Historicametics and the Best own and information fractitude. When are not restrictions on its most for any profit is matrix to as songed a tisse contained for immerity entities a license agreement (see http://www.isb-sib.ch/announce/or send an easil to licensesiab-sib.ch).
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Immunogalboulin domain, GPL-anchor;
Alternetive splicing; 3D-structure.
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EXTRACELLULAR (POTENTIAL).
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-:- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-:- SIMILARITY: CONTAINS I IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-:- DATABASE: NAME-PROW; NOTE-CD quide CDS8 entry.
WWW-THIEP://www.ncbi.nlm.nlm.gov/prow/cd/cd88.hlm*.
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Pred. No. 2.5e-106;
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BRIEF, MUSSES CA
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NEDLINE-91133857; PubMed-1999350;
Rorlhok V., Stefanova I., Mapellsova P., Hilbert I., Horejsi V.;
Tythe human Jeucocyte antigen CD48 (MRM-102) is closely related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDE-----DEVEMESPNITDTMK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TKIAKFKNG---SWTPQKDKTYEVLKNGTLKIKHLERIHEGTYKVDAYDSDGKNVLEE-T 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 PPLYVLESLPSP-----TLTCALTNGS-IEVOCMIPEH--YNSHRGLIMYSWDCPM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 FHLSLLEMVSKPNISWSCTNTTLTCEVTKGTDFELKLYLNGRMIOKSPRKVIVY----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                      CYTOPIASHIC (POTENTIAL).
101-LIKE V-TYPE DOMAIN.
101-LIKE C2-TYPE DOMAIN.
3 X 7 AA TANDEM REPEATS OF H-R-P-[0L]-
(AVP)-P-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO-RECH
PRO-RECHEMENT MACHINE (PORBETTAL)
PRIME GLANGE ... (PORBETTAL)
PRIMED GLANGE ... (PORBETTAL)
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Mommalla; Eurheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TRAID=6606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
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Sandrin M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72; Indels
                                                                               T-CELL SURFACE ANTIGEN CD2
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 ---KRASNQI-----ASPKCTANNTVSEESSSVVI 197
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                                               BY STMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA clones for CD48.
                                                                                                                                                               POTENTIAL
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Immunogenetics 33:113-117(1991).
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Immunogenetics 33:108-112(1991).
               Signal
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347 AA;
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       Cell adhesion;
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P09326;
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                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 STKTIFESEFKGRVYLEENNGALHISNVRKEDKGTYYMRVLRETENBLKITLEVFDPVPK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1 PSIEINKTEASTDSCHLRLSCEVKDQH------VDYTW-----YESSGPF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 PKKSPGYULDLIVTPONKSTFTTCOVSNPVSSKNDTV-----YFTLPCDL 214
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                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             59 SEFRAF-SSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDT-MKFFLYVLESLPS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 PILTCALINGS----IEVOCMIPSHYNSHRGLIMYSWDCPMEOCKRNSTSIYFKMENDL 181
                                                                                                                                                                                                                                                                                      13 VLSVVCLLHCFGFISCFSQQIYGVVYGNVTFHVPSNV--PLKEVLWKKQKD-KVAELE-N 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISSP; P06729; 1GYA.
(mmunoqlobulin domain; T-cell; Glycoprotein; Antiqen; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                             11 VLELLLLPLGTGFQGHSIPDINATTGSNVTLKIHKDPLGPYKRITWLHTKNOKILEYNYN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              histories (1981).
Tavernor A.S., Kydd J.H., Bodian D.L., Jones E.Y., Stuart D.L.,
Davis S.J., Butcher G.M., "Expression cloning of an equine T-lymphocyte glycoprotein CD CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotas, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
203 203 N-LINKED (GLCNAC. . .) (POTENTIAL)
240 AA, 27383 MM; F3BE6987A9E9C71E CRC64;
                                                                                                                                                                                                      77;
                                                                                                                               DB 1; Length 240;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                      90
                                                                                                                       Match 9.9%; Score 131.5; DB 1
Local Similarity 21.9%; Pred. No. 0.00032;
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15-JUN-2002 (Rel. 41, Last annotation update)
T-cell surface antiqen CD2 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 AA
                                                                                                                                                                                                      36: Mismatches
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                                                                                                                                                                                                      57; Conservative
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15-JUN-2002 (Rel.
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P37998;
       SEQUENCE
                                                                                                                               Query Match
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us-09-730-465-2.rsp

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Diamond D.3. Clayfon L.K., Sayte P.H., Reinherz E.L.;

John Litton organization and Sequence comparison of human and murine error. Natl. Acad. Sci. U.S.A., 85:1515-1619(1988).
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MEDINE-89005055; PubMed-2801953)
Crumpton M.J., Kloussis D.;
Crumpton M.J., Kloussis D.;
The structure of the imman CD2 gene and its expression in transgenic mice.;
                                                                                                                                                                                                                                                                                     143 MIP-EHYNSHEGLIMYSW---DCPMEOCKRNSTSIYEKMENDLPOKIOCTLSNPLFNTTS 198
                                                                                                                                                                                                                                                                                                                                                                 155 VIPGESVN-----YTWYGDKRPPPKELONSVLETTLMPHNYSRCYTCQVSNSVSSKNG 207
                                                                                                                                                                                                         95 YISKVOKEDNSTYIMRVLKKTGNEQEWKIKLQVLDPVPKPVIKIEKIEDMDDNCYLKLSC 154
01-37M-1998 (Rel. 06, Created)
15-00-1986 (Rel. 06, Lorested)
15-00-1986 (Rel. 09, Last sequence update)
15-00W-2002 (Rel. 41, Last ennotation update)
15-01W-2002 (Rel. 41, Last ennotation update)
17-04L suffice antique Of Preduzeo (Trell suffice antique neceptor) (Rell suffice antique (Rell suffice antique) (Rell suffice)
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Rokaryota, Wetazoa; Chordata; Craniata; Vertabrata; Euteleostomi;
Memmalia; Euteleis; Primates; Catarrhini; Nominidae; Nomo.
NCBL?axine506;
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MEDLINE-87041525; Pubmed-3490670;
SEGELI M.A., BECOM M.H.J., Dunne J., Oven M.J., Crumpton M.J.;
*Molecular cloning of the human T-lymphocyte surface CD2 (TII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HERDINGER FROM IN. PRUMACH 21375.
HERDINGE TOWN IN. PRUMACH 21375.
"PAGE B. ATHICK CALDINGS OF the CDS antigen, the T-cell stythrocyte receiver in a rapid immunosefaction procedure".
From the Acad. Sci. U. S. A. 813165-3150[1987].
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roc. Natl. Acad. Sci. U.S.A. 84:7256-7256(1987).
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MEDLINE-88144486; Pubmed-2894031;
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P06729:
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REMOVED IN MATURE FORM.
GPI-ANCHOR.
                                                                                                                                                                                                                                                                                                                       MEDINE-91141511; PubMed-1801502; PubMed-180150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: LIGAND FOR CD2. MIGHT PACILITATE INTERACTION BETWEEN ACTIVATED LYMPHOCYTES, PROBABLY INVOLVED IN REGULATING T-CELL
                                                                                                                     Staunton D.E., Thorley-Lawson D.A.; "Molecular cloning of the lymphocyte activation marker Blast-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00047; 1g; 1; 38ART; SM00049; 1G: 1; 1mmuno49; 1G: 1; 1mmuno45; 1G: 1; 1d: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9E46D76FC36A512C CRC64;
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N-LINKED (GLCNAC...
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I -> N (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.3%; Score 123;
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                                                                                    MEDLINE-88111558; PubMed-2828034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE.
MEDLINE-91237281; PubMed-1827826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of human chromosome 1.";
J. Exp. Med. 173:1339-1344(1991).
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EMBL; X06341; CAA29647.1; -.
EMBL; M37766; AAA36211.1; -.
EMBL; M63911; AAA35602.1; -.
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PIR; A53244; A53244.
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es 50; Conserv
                                          SECUENCE FROM N. A.
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Matches
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EMBO J. 7:1675-1682(1988).

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Gaps

79: Indels 24:

36 VVYG-NVTFHVPSNVP--LKEVL#KQKD-KVAELENSEFRAF-SSFKNRVYLDTVSGSL 90

Conservative

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90 -----GTLKIKHLKTDDQDIYKVSIYDTKGKNVLEKI-FDLKIQERVSKPKISWTCINF 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 TLTCEVMNGT-----DPELNLYQDGKHLKLSQRVITHKW-----TTS----- 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 YLDTVSGSLTIYNUTSSDEDEYEM----ESPNITDIMKFFLYVLESLPSP----- 127
                                                                                                             finanunogiobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;
Cell adhesion; Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO-CITCURE 1 MINIMO, SELLON 4.

PER SYMILARITY.

PER SYM
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IG-LIKE C2-TYPE DOMAIN.
LFA-3 (CD58) BINDING REGION
LFA-3 (CD58) BINDING REGION
                                                                                                                                                                                                                                  T-CELL SURFACE ANTIGEN CD2
                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
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Genew; HGNC:1639; CD2.
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                                                                                                                                                                                                                                                                                             MEDLINE-94348865; PubMed-7915183;
Withka J.M., Myss D.F., Wagner G., Arulanandam A.R.N., Reinherz E.L.,
                                                                                                                                                                                                                                                                                                                                                                                                   "Structure of the glycosylated adhesion domain of human I lymphocyte
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MEDIATURE-9531045; PORMON-254449;

NOTABROWN OF ALL ALL ALL AND ORDER M.M. WILLIE K.J.,

KNIMBARDIAM A.K., SEROYA A.K., MEDIATURE A.L., NARROW C.J.,

SOLIC A.R., MEDIATURE A.K., MEDIATURE A.K.
                                                                         Boddan D.L., Jones E.Y., Harlos K., Stuart D.I., Davis S.J.;
"Crystal structure of the extracellular region of the human cell
adhesion molecule CD2 at 2.5-4 resolution.";
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-1- SIMILARITY: BELONGS TO THE IMMUNGLOBULIN SUPERFAULT.
-1- SIMILARITY: COUTAINS I IMMUNGLOBULIN-LIKE V-TYPE DOMAIN.
-1- SIMILARITY: COUPAINS I IMMUNGLOBULIN-LIKE 02-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE-880359775, PubMed-2444890;
seteraron A. Seed B.,
Wonoclonal antibody and ligand binding sites of the T cell
scythnooge receptor (DZ).;
Meture 339:842-846(1987).
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WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd2.htm".
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 25-206
MEDLINE-95086863; PubMed-7994575;
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X07874; CAA30721.1; JOINED.
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                                                                                                                                                                                      Structure 2:755-766(1994).
                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 25-129.
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PIR: S00829; S00829;
PDB: 1LDB: 15-OCT-94.
PDB: 1HNF; 07-FEB 95.
PDB: 1GYA; 08-NOV-96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 ----IEVQCMIPEHYNSHRGLIMYSW-----DCPMEQCKRNSTSIYFKMENDLPQKIQC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : | : | : | 374 DGICRISLITCSVEDGGGTT----VMYTWTPLQKEAVVSQGGSHLAVSWRSSENH--PNLTC 427
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                                                                             (POTENTIAL)
                                                      ( POTENTIAL)
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       (POTENTIAL)
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Ekkaryota: Vungi Ascomycus: Schizosaccharomycetes;
Skikzosaccharomycetales; Schizosaccharomycetaces;
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10.-FEB-1996 (Rel. 31, Last sequence update)
13-JUN-2002 (Rel. 41, Last annotation update)
19-DUN-2002 (Rel. 41, Last annotation update)
FEB-1996 (Treated) protein CIFS-07c in chromosome I.
                                                                                                                                                                                                                                                                                                                             8.5%; Score 113; DB 1
20.8%; Pred. No. 0.042;
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Warkerie I.F. Warkerie I.F. 
*1solation and characterization of cDNA clones for Huming's the human 
*1solation and characterization of cDNA clones for Huming's the human 
Immunogenetics 43:13-19 (1996).
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MODINE-20474510: PubMed-10970093.

MODINE-20474510: PubMed-10970093.

FROM Y., de B. NE FROMER M. P. Bitchela P., Bosech J., Engel P.; Green structure of the mouse leukocyte cell surface molecule Ly9.*;
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**Subscriptura Location**, Type I se
15-JUN-2002 (Rel. 41, Last annotation update)
7-lymphocyte surface antique Ly-9 precursor (Lymphocyte antique 9)
(Cell-surface molecule Ly-9) (CD229 antique).
                                                                                                                                                                                                 Bukaryota, Wetazoa; Chordata; Graniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxip-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
M-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal, Transmembrane, Glycoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASHIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE CZ-TYPE DOMAIN 2.
IG-LIKE V-TYPE DOMAIN 2.
IG-LIKE CZ-TYPE DOMAIN 2.
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The propaga (1)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96128248; PubMed-8537117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenetics 51:788-793(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-151 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:6730; LY9.
MIM; 600684;
                                                                                                                                                                  Homo Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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This SMIS-SYOT entry is opergright. It is produced through a collaboration between the SMIS institute of Incidentation and the BRBL outtration. The Bangean infolioration lengthstatute. There are no restrictions on its modified and that attendant thome remove the content of many modified and that attendant thome removed. The second of the second entries removed a place obstantial to memorable mentities returned a little statement is of the second 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 VVLNQLTAEDEGFYWCVSDDDESLTTSVK--LQIVDGEPSPTIDKFTAVQGEPVEITCHF 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PCKYFSSEK-----YW-----CKWNDHGC-----EDLPTKL--SSSGDLVKCNNNLVLT 522
       ABSOLAPERA, SHRFALE OF BTTHELLAL CELLS, THE COMPLEY IS THEN THANSONED ACROSS THE CELL TO BE SECRETED AY THE APLCAL SURFACE DURING THIS PROCESS A CLAMAGE OCCURS THAT SERAMENE THE TRANSCHELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE TRANSCHEBBANE SCRAEFY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. ..); IN ALLOTYPE T61.
N-LINKED (GLCNAC. ..); IN ALLOTYPE T62
(FARTIAL) AND T63.
N-LINKED (GLCNAC. ..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GNVTFHVP----SNVPLKEVLWKKOKDKVABLENSEFRAFSSFKNRVYLDTVSG----S 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVDQLTON -> YINRLSQS (IN ALLOTYPE T61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO SECRETED. POLYPORPHISM: THE SUGUENCE SHOWN IS THAT OF ALLOTYPE TG2. SIMILARITY: BELONGS TO THE IMMUNOSLOBULIN SUPERFAILY. SIMILARITY: CONTAINS FIMONOSLOBULIN-LIKE V-TYPE DOMAINS.
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IG-LIKE V-TPE DOMAN 1.
IG-LIKE V-TPE DOMAN 2.
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IG-LIKE V-TPE DOMAN 4.
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IG-LIKE V-TPE DOMAN 5.
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D -> E (IN ALLOTYPE 761).
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2.0%; Pred. No. 0.2
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773 AA;
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Natches 47; Conserva
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                                                                                                     THE SMISS TOWN CHELT IS COPYLIGHT. IT IS produced through a collision between the suss institute of lioinformatics and the BML outstation. The European halfoldsometical faithtings of these are no restrictions on its modified and this stringent through a continue to the superior and the superior and the superior and the superior allocate and engagement (see http://www.isb-sib.ch/ancounce/or and an exail to Licensedis-bio.).
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15.7UR-1996 (Rel. 01, Lest enquence update)
15.7UR-2000 (Rel. 41, Lest enquenciation update)
15.7UR-2000 (Rel. 41, Lest enderistion update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 FGFLAKIEKK-----YGNITLGLIRALLAREILSPAEKALKAALLABPKTAELSNS-MKS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 FSSFKNRVYLDTVSGSLTIXNLTSSDEDEYEMESPNITDTMKFFLYVLESLPSPTLTCAL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 TSMFAFKEGIETI-----TLSIADELK-KMPNV----KIHL----NKPAKTLVPHK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 TNGSIEVOCMIPEHY --- NSHRGLINY SWDCPMEOCKRNS --- TSIYFKMENDLPQK --- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 TOSLVDVNGQAYEYVVFANSSRNLENLI-SCPKMETPISSVYVVNVYKKDPNVLPIRGFG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 LLIPSCIPNNPHPULGIVFDSEQNNPENGSKVTVMMGGSAYTKNT-SLIPTNPEEAVNNA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 FGFISCFSOQIYGVVYGNVTFHVPSNVPLKEVLWKKQK------DKVAELENSEFRA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLING-TROWN 4/12245: Purbled-6/32002;
WESTOW K.E., Friedlander M., Blobel G.;
Westow K.E., Friedlander M., Blobel G.;
The receptor for transperitetial transport of 19A and 19A contains multiple immunoglobulin-like domains.';
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INGLINES-STREET, THE STREET, THE STREET STREET, THE STREET STRE
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-!- SIMILARITY: TO PROTOPORPHYRINGGEN OXIDASE (EC 1.3.3.4) AND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 106; DB 1; Length 490; 23.9%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Přám: Př01593; Amino_oxidaše; l.
TRTRAMA: TXR08058; proto_IX_ox; l.
Bypotherical protein.
SEQUENCE 490 AA: 53461 NW: CB679F6AA37547AA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002937; Amino_oxidase.
IPR004572; Proto_IX_ox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 VLYMNGILKCDRKPDRTNS 249
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P01832;
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Murray A.J., Head J.G., Barker J.J., Brady R.L.; Head assembly.";
*Figitneering an intertwined form of CD2 for stability and assembly.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Būkaryotai Mētazoa; Chordata; Cranlata; Vertebrata; Buteleostomi;
Bammalia; Buthbata; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
NCBI_TWATI=0116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams A.F., Barciay A.M., Clark S.J., Paterson D.J., Willis A.C., Samilarties in sequences and cellular expression between rat CD2 and CD4 antigens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE-68437862: PubMed-2901253;

WEDLINE-68437862: PubMed-2901253;

"A role in transmembrane signaling for the cytoplasmic domain of the Taylor 2T lymbhogres mixtoe antiqen.";

Cell 54:397-984(1988);
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"Crystal structure at 7.8" A resolution of a soluble form of the
adhesion molecule (D2.)".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01:WOV-1986 (Rel. 09, Created)
10:WOV-1986 (Rel. 09, Last sequence update)
11:WOV-108 (Rel. 14), Last sequence update)
12:WOV-108 (Rel. 41), Last sequence update)
13:WOV-108 (Rel. 41), Last sequence (Rel. 18) surface antigen
111/Lear-5) (LRN-3 (LRN-3 Exceptor) (QX-34 antigen).
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"One sequence, two folds: a metastable structure of CD2.";
Proc. Natl. Acad. Sci. U.S.A. 92:7337-7341(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barclay A.N., williams A.F.;
Submitted (MAY-1987) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 42-344 FROM N.A., AND PARTIAL SEQUENCE
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X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 23-198.
MEDLINE-93063364; Pubmed-1279440;
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MEDLINE-95365363; PubMed-7638192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 AA
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                                                                                                                                                                                                                                         221 IPLAVITECIV 231
                                                                                                                                                                                                                                                                                               229 VILSTIPSILL 239
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P08921;
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- SHILLANTE BLOAKS OF THE PHONOCACHAINS SPERSHALDS.

SHILLANTE CONTAINS I DMENNOCLOBELLS-LIKE CT-TPEP DOMAIN.
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                                                                                                                                                                                                     01-4487-1969 (Ret. 10, Created)
101-4487-1969 (Ret. 10, List; sequence update)
115-0108-2002 (Ret. 11, List; sequence update)
115-0108-2002 (Ret. 11, List; and precursor (ROML surface antigen) (BLAST-1)
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Killeen W. Mossener R. Avrient S. William A. Williams A.F.;
Ne Cover and Apple of Creat Annocytes and endochellum is in a
contented of the Cover of the Creat Annocytes and endochellum is in a
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- Profession: Lidean Post Cox, NIGHT PACLITANE, PREMIUM DESCRIPTION.
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                                                                                                                                                                                                                                                                                                                                                                                         Ratus norvegicus (Rat).
Kadraryota: Metazos: Chordata: Craniata: Vertebrata: Buteleostomi;
Mammalia: Butheriaza Rodentia: Sciurognathi; Murides, Murinae; Rat
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523 LTLDSVSEDDEGWYWCGAKDGHEFEEVAAVRVEL 556
                                                                                                                                                     240 AA
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GlycoSuiteDB; P10252; -.
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as 55; Conserv
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                                                                                                                                               CD48_RAT
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52 NISIDELARMRIYWOKDOOWVLSIISGOVEVWPEYKNRTFPDIINNLSLMILALRLSDKG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 EY-----EMESPNITDIMKFFLYVLESLPSPT---LTCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 TYTCVVOKNENGSFRREHLTSVTLSIRADFPVPSITDI-----GHPDPNVKRIRCS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 LINGSIEVOCMIPEHYNSHRGLIMYSWDCPMEOCKRNSTSIYFKMENDLPOKIOCTLSNP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 ASGG------PPEP------RLAWMEDGEELNAVNTTV----DODLDTELXSVSSEL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 LFNTIS--SIILTICIPSSGH-----SRHR----YALIPIPLAVITTCIV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunojioutin domain; Freeli; Glycoprotein; Signal; Transmembrane; Receptor.
                                                                                                                                                                                                     THE TRANSPORT OF THE COSTINUIANORY SIGNAL ESSENTIAL FOR T INVESTOR; INVOLVED IN THE COSTINUIANORY SIGNAL ESSENTIAL FOR T INVESTOR; INVOLVED IN THE SHOLD FERRATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CDS OR CTLA-4 TO THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W.LIWED GLOMAC (POTBETAL)
W.LIWED GLOMAC (POTBETAL)
W.LIWED GLOMAC (POTBETAL)
W.LINED GLOMAC (POTBETAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T LYMPHOCYTE ACTIVATION ANTIGEN CD80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70; Indels 87;
                                                                                                                                                                                                                                                                                                                        -: SUBCELLURAR LOCATION: Type I membrane protein.
-: SIMILARITY: BELOKGS TO THE IMMUNGCLOBULIN SUPERSAMILY.
-: SIMILARITY: CONTAINS I IMMUNGCLOBULIN-LIKE C-TYPE DOMAIN.
-: SIMILARITY: CONTAINS I IMMUNGCLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%; Score 92.5; DB 1; Length 299;
9.4%; Pred. No. 0.91;
                                                                                                                                              Isono T., Seto A.; 
'Cloning and sequencing of the rabbit gene encoding T-cell
    Mammalia: Eutheria: Lagomorpha: Leporidae: Oryctolagus
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6744223E5CC91DE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                           STRAIN-B/J X CHBB:HM;
MEDLINE-95369849; PubMed-7642234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; IG.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003600; Ig.like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33513 NW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D49843; BAA08643.1; -. HSSP; P33681; 1DR9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.48;
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SWART; SW00409; 1G; 1.
SWART; SW00410; 1G_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.0%
Best Local Similarity 19.4%
Matches 47; Conservative
                                                                                                                                                                                       costimulatory molecules.
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185
206
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299 AA;
                                                                         SECURNCE FROM N.A.
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                                                                                                                                                                                                     This SHIES STORY entry is expected. The produced through a collaboration between the state institute of inclinionation and the EMEL contraction the buryone principlement in section of the region of perficience of the expected of the production of the modified and this statement is not removed. Using the principle of the statement is not removed. Using the py and for commercial entry as illusions approached to the production of the commercial contraction of the production of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 GSLTITMLISSDEDEYEME - SPNIIDIM - KFFLYVLESLPSP - - - - - ILICALT 134
ANTIGEN (LEA-3) AND OX-45/BCM-1 TO MEDIATE ADHESION BETWEEN T
CELLS AND OTHER CELL TYPES. CD2 1S INFLICATED IN THE TRIGGERRING
OF T-CELLS, THE CYPOLASHIC DOMAIN IS IMPLICATED IN THE
SIGNALING FORVION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IRR005800; Ig_like.
SAMT: SOOULO, [3.1]ke.]
Immunostobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;
Cell adhesion; Repeat; Signal; 30-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 GVVYGNVTFHVPSNVP-----LKEVLMKKQKDKVAELENSEFRAFSSFKNRVTLDTVS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 GTVWGALGHGINLNIPNFOMTDDIDEVRWERGSTLVAEFKR-KMKPF--LKSGAFEILAN 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 NGSIEVOCMI---PEHYNSHRGLIM-YSWD---CPMEQCKR-NSTSIYFKME-NDLPQK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     f lymphocyte activation antigen CD80 precursor (Activation B7-1
                                                                         SIGNALINE PROFILED TAPE

SUGCELLULAR MOCATION: Type I membrane protein.

SIMPLARITY: BELLARITY SIGNANGS TO THE MUCHOCLOBULINE LIKE VIPE DOMAIN.

SIMILARITY: CONTAINS I HEROMOCLOBULINE LIKE C2-TIPE DOMAIN.

SIMILARITY: CONTAINS I HEROMOCLOBULINE LIKE C2-TIPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.3%; Score 97; DB 1; Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-CELL SURFACE ANTIGEN CD2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
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IG-LIKE C2-TYPE DOMAIN.
PRO-RICH.
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15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38414 MW:
                                                                                                                                                                                                                                                                                                                                                                                        ZMBL; X05111; CAA28757.1; -.
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PIR; A32346; A32346,
PDB; LCDC; 15-SEP-95,
PDB; ILNC; 07-FEB-95,
PDB; 1A64; 27-MAY-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1A6P; 17-JUN-98.
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134
344 AA;
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P42070;
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108 KVSEDGYSLYMSNLTKSDSGSYHAQINOKNVILTTNKEFTLHIYEKLOKPOLIVESVTPS 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 DIDSCIPT----LICTVKGTKDS----VOYSWTREDTHLNTYDGSHTLRVSOSV---CD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 YLDTVSGSLTIYNLTSSDEDEY--ENESPNI--TDTMKFFLYVLESL------PS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 IYGVVYGNVTF-----HVPSNVPLKEVLMKOKDKVAELENSEFRAFSSFKNRV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoal, Mammaila, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Cell adhesion; Antigen; Signal; Transmembrane; Glycoprotein; 
Thamtoglobulin domain; Repeat; Polymorphism. 
SIGNAL 1 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.9%; Score 91; DB 1; Length 654;
4.4%; Pred. No. 3.2;
                                                                                                 T-LYMPHOCYTE SURFACE ANTIGEN
                                                                                                                                                                                                                                     IG-LIKE V-FPE DOMAIN 1.
IG-LIKE C2-TPE DOMAIN 1.
IG-LIKE C2-TPE DOMAIN 2.
IG-LIKE C2-TPE DOMAIN 2.
POTENTIAL.
POTENTIAL.
                                                                                                                                    EXTRACELEULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC...) (F. N-LINKED (GLCNAC...) 
                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 PDLP--YTCKAWNPVSONSSOPVRIWOFC---TGASRRKTA
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15-701-1999 (Rel. 38, Late Sequence update)
15-701-1999 (Rel. 40, Late annotation update)
PRT: 10 Corr. 2001 (Rel. 40, Late annotation update)
PRT: 10 PRT: 10 Create
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REDLINE-2217905: Pubmed-190666.

REDLINE-2217906.

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Gene structure of the mouse leukocyte cell surface molecule Ly9.";
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Enkaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
MCBL Taxil-10090;
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STRIN-129/5v. AMLB/c. and CSTBLIN-16: TISSUE-Spleen:
MDLINE-204.24510; PubMed-10970093;
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AF246699; AAG13268.2; JOINED.
AF246700; AAG13268.2; JOINED.
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InterPro; IPR003606; Ig_1ike.
Pfam; PF00047; Ig; 3.
SAMRT; SM00409; IG; 2.
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HSSP; P08921; 1HNG.
MGD; MGI:96885; Ly9.
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white SMISS-FORT entry is copyright. It is produced though a collaboration between the SMIS institute of Bioinformatics and the BME outstation. The Brongest Bonichmantities Institutes "Three are no restrictions on its modified and this streamt is once the conference of the streamt is one removed. Blue or other and for commercial entities removed a like to commercial entities a license agreement (see http://www.isb-iib.ch/nmonnecy or send an unit to licensefabs-iib.ch).
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tissue-specific expression and evolutionary relationship with the
low-density-limoprotein research.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus
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Eur. J. Biochem. 224:975-982(1994).
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MEDLINE-95010090; PubMed-7925422;
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MEDLINE-95003355; PubMed=7919660;
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-- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED G-TERMINAL (PAC) DOMAIN.
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25.0%; Pred. No. 6.8;
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MEDLINE=98318231; PubMed=9655499;
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InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS domain.
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1- SINGELLULIAR LOCATION: Type 1 membrane protein.

1- TISSUE SERETECTETY: TRANSMATH IS ADDISI GAFFACENRULUS, HEART HEAST LACERY, SRAIM, LUNK AND HAITE FAT. LESS IR ADERA, OMRAY, ROLLE, PLACERY, SELEM, ADDISANG CHAND, ADDIAINS.

1- SINILARIY: COWNAINS & LOL-REDEPTOR CLASS, DOMAINS.
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HObbs H.H.;
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01-007-1996 (Rel. 34, Last equence update)
15-JUN-2007 (Rel. 41, Last annotation update)
15-JUN-2007 (Rel. 41, Last annotation update)
Very low-density lipoprotein receptor precursor (VLDL receptor).
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LD. PREPROFE (CASE AL)
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GenCore version 5.1.3 Copyright (c) 1593 - 2003 Compagen Ltd. Of protein - protein search, using sy model and the compage of t	(without alignments) 976.271 Willion cell updates/sec Title: US-US-730-465-2 Septence: U30 WANSENGRALTVLSYVULVLRWGILKIDREPRENS 250	Scoring table: Unicated Gapop 11.0., Gapop 11.0., Gaport 0.5 Searched: (7)1880 seep, 206047115 residues	Total number of hits satisfying chosen parameters: 671380 Maximum Da seq length: Ontononon Maximum Da seq length: Ontononon	Note: processing Miliams Watch 0s Maxims Match 0s Maxims Match 0s Maxims Match 10s Listing first 4s summaries	Outshape : Symposite (21: *) Symposite (21:	98 90-20 granual lat- 10 90-20 granual lat- 11 90-20 granual lat- 12 90 y Virus: 13 90 y Virus: 14 90 y Virus: 15 90 y Virus: 16 90 porter (sep. 17)	Pered No. is the number of results predicted by chance to have a case spatied to a case of priced of the cost of the result being printed, and is derived by analysis of the total more distribution, printed by analysis of the total more distribution. SIMMAKIES FROM! No. Score Match Length DB 1D Description	124 9.19 9.10 4 (1989) 101

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61 DKVAEL-ENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLY 119
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                                                                                 42.44; Score 562; DB 4; Length 119;
57.04; Pred. No. 6.7e-46;
ive 0; Mismatches 1; Indels 88; Gaps
                                                                                                                                                                                                                                                                                                     37 VYGNVTFHVPSNVPLKEVLMKKQKDKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLT 96
                                                                                                                                                                                                                                                                                                                                                        1 YYGNVTEHVPSNVPLKEVLWKKQKDKVAELENSEERAFSSFKNRVYLDTVSGSLTIYNLT 60
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
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Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases
EMBL, D28584; BAA05920.1; --
HSSP; P19256.10CZ.
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4096AC6F45181505 CRC64;
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01-809-1596 (TEPBHIRE). 01, Created)

01-809-1596 (TEPBHIRE). 01, Last sequence update)

01-BE-2001 (TEPBHIRE). 19, Last annotation update)

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PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1
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13732 MW:
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es 118; Conservative
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119 AA;
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                                        181 LPOKIQCTLSNPLRNTTSSILLTTCIPSSGHSRHRYALIPIPLAVLTTCIVLYHNGI 237
18 LPOKIQCTLSNPLRNTTSSILLTTCIPSSGHSRHRYALIPIPLAVLTTCIVLYHNGR 237
18 LPOKIQTTLSNPLRNTTSSILLTTCIPSSGHSRHRYALIPIPLAVLTTCIVLYHNGR 237
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NGBL_faxiD=9606;
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Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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Matches 134; Conservative
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RESULT 5

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61 DKAVEWEBOYNVTAPPPFVDRVHLATGSGDLTIYNFAFEDBGDYQIESPSVKNSSKFILR 120
61 DKVAELENS-EFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMBSPNITDTMKFFLY 119
                                                                                                                                                                                   120 VLRSI,PSPTLTCALTNGSIRVOCMIPEHYNSHRGLIMYSWDCDME---OCKRNSTSIYFK 176
                                                                                                                                                                                                                                                                         121 VVEPLPEPELYCESTEGNISVRCLILAASLRHIDLIOYSWNCPPTVSCOAGLGPSEMYIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DKVAEL-ENSERAFSSFKNRVYLDTVSGSLTIYNLTSSDEDBYEMBSPNITDTMKFFL- 118
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Cham S. W. S., Widdleton D.L., Landquist M., Warr G.M., Biggins D.A.;
"Assa platypropen T coll antigens";
Submitted (ARR-2001) to the BABL/GenBamk/Dobd databases.
BABL, NO02731; AAMS1607.1: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRA-3(delta D2) precursor.
Ovis 8 ps.
Rikaryotis Metazos, Chordata; Craniata; Wertebrata; Buteleostomi;
Memmalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anas platyffynchos (Domestic duck).
Ekkaryota; Marcas (Domestic duck).
Archosauria; Aveza, Rognerhab; Anseriicomes; Anatidae; Anas.
                                                                                                                                                                                                                                                                                                                                                                       177 MENDLPQKIQCTLSNPLFNTTSSIILTTCIPSSGHSRHRYALIPIPLAVITTCIVL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.6%; Score 326.5; DB 6; Length 159;
45.4%; Pred. No. 2.6e-23;
tive 22; Mismatches 52; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kakutani T.;
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases
BMBL, DBSBS; BAAGS10-1;
HSBP; P19256; ICCZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592A97046ECD985E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VIDYARHRYULFAI-LPAVIC----GLLFLKCFLGRRSORNSG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               יבייטט' (TrEMBLrel, 19, Last sequence update) 01-MAR-2002 (TrEMBLrel, 20, Last annotation update) CD58 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 22; Mismatches
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBL_TaxID-9939;
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Q28752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKVAEL-ENSEFRAFSSFKNRVXLDTVSGSLTIYNLTSSDEDEXEMESPNITDTWKFFLX 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 VLESLPSPTLTCALT-NGSIEVQCMIPE---HYNSHRGLIMYSWDCPME-QCKRNSTS-- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVAGSDAGRALGVLSVVCLHCFGFISCFSQQIYGVVYGNVTFHVPSNVPLKEVLMKKOK 60
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                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
Bukaryota, Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Metazoa: Chordata; Animaryola; Suina; Suinas; S
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Brossay A., Hube P., Bardos P., Watter H.;
Characterization of the porcine CDSB antigen mRNA sequence.";
Sibmitted (ANA-2001) to the EMBL/Gensank/DDBJ databases.
EMBL: AF469666; AAA16578.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.0%; Score 517.5; DB 6; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.2%; Score 453.5; DB 6; Length 244; 40.7%; Pred. No. 3.4e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
EMBL: D28585; BRA05921.1; -.
HSSP; P19256; LCCZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEA-3(DELTA TM).
1521A800849E9R55 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 IYPKMENDIPOKIOCTLSNPLFNTTSSIILTTCIPSSGHSRHRYA 217
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                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DSC-2001 (TrEMBLrel. 19, Last annotation update)
LFA-3(delta TW) precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 2.5e-41;
34; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 AA.
                                               227 AA
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01-JUN-2002 (TERBirel. 21, Created)
01-JUN-2002 (TERBirel. 21, Last sequ
01-JUN-2002 (TERBirel. 21, Last anno
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                                               DRT:
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29 227 LE
227 AA; 24760 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sest Local Similarity 48.9%;
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                                               PRELIMINARY
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90 -----GTLKIKHLKTDDQDIYKVSIYDTWGKNVLEKI-FDLKIQERVSKPKISWTCINT 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 TLTCALTNGSIEVQCMIPE-----HYNSHRGLIMYSWDCPMEQCKRNSTSIYFKMEN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 TLTCEVMNGT-----DPELNLYODGKHLKLSORVITHKW-----TTS----- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 DLPQKIQCTLSNPLFNTTSSIILTTCIPSSGHSRHRYALIPI-----PLAVITTCIVLYM 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 -LSAKFKCTAGNKV-SKESSVEPVSC-PEKG--LDIYLLIGICGGGSLLAVPVALLVFY] 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.2 FTWGALGODINLDIPSFONSDDIDDIKWEKTSDKKKIAOFRKEKFKEKDTYKLFKN-- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 QIYGVYYGNVTFHVPS---NVPLKEVLWKKQKD--KVAEL--ENSEFR---AFSSFKNRV 81
                                                                                                                                                                                                                                           Eukaryota Metazoa; Chordata; Cranlata; Vertebrata; Buteleostoml; Mammalia; Eurheria; Primates; Catarrhini; Hominidae; Homo. WCBI_TARID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        8.7%; Score 115.5; DB 4; Length 351;
23.0%; Pred. No. 0.0084;
ive 42; Mismatches 76; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Villinger F., Bostlk P., Mayne A.E., King C.L., Genain C.P.,
                                                                                                                                                                                                                                                                                                                                             HB11 R.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL ALIS598: CAC14840.1; -- SEQUENCE 351 AA; 39448 MM; A03D853C3B618917 CRC64;
                                                                                           Offices.

01-08C-2001 (TEPBELEA. 19, Created)
01-08C-2001 (TEPBELEA. 19, Last sequence update)
01-108-2002 (TEPBELEA. 21, Last annotation update)
01-108-2002 (TEPBELEA. 21, Last annotation update)
04-55815-1 (CD2 antigen (p50), sheep red blood cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLRE). 01, Created)
01-NOV-1996 (TREMBLRE). 01, Last sequence update)
101-UNK-2002 (TREMBLRE). 21, Last aminication update)
17 procein (CD00 protein precursor).
                                                                               351 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 AA
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ses 59; Conservative
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                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                   Homo saptens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning, characterization, and chromosomal localization of
the mouse homologue of CD84, a member of the CD2 family of cell
surface molecules.";
                                                                                                                                                                              22 IYC-BEKVEGILGENETPPVKADNKIDEVIAPKDKDKVAEWEAGSEPTYENSLESBSILLN 80
                                                                                                                                                                                                                                   85 TVSGSLTIYNLTSSDEDEYEME---SPN1TDTMKFFLYVLESLPSPTLTCALINGSIEVO 141
                                                                                                                                                                                                                                                                         81 KESGNLTIPKLENSDSGMYHLERFSSRTENGVPTFNLTVLDPPSEPQINCSLSDDNLMLT 140
                                                                                                                                                                                                                                                                                                           142 CMIPEHYNSHEGLIMYSWDCPMEGCKRNSTSIYFKMENDLPOKIOCTLSNPLPNFTSSII 201
                                                                                                                                                                                                                                                                                                                                                 141 CEA-----KFORPLTYVWKITGREIFTGPKVL1PKENVDTGGKATGFVTYFKMTKSSELT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 GSLTIYNLTSSDEDEYEM---ESPNITDTMKFFLYVLESLPSPTLTCALTNG----SIE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 YDLV1RDLRMEDAGTYKADINEENEETITK1YYLHIYRRLKTPKITQSLISSLNNTCNIT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 VQCMIPEHYNSHRGLIMYSWDCPMEQCKRNSTSIYFKMENDLPQKI--QCTLSNPLFNTT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 LTCSVEKERKD----VTYSWS-PFGE-KSNVLQI---VHSPMDQKLTYTCTAQNPVSNSS 200
                                                                                                                 15; Gaps
                                                                                                                                                           26 1SCFSQQ1YGVYGNVTFHVPSNVPLKEVLWKKQKDKVAELE-NSEFRAFSSFKNRVYLD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 GVVYGNVTFHVPSNVPLK -- EVLHKKOKDKVAELENSEFRA-----FSSFKNRVYLDTVS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 GILGESVIFLLNIQEPKKIDNIAWTSQ-SSVAFIKPGVNKAEVIITQGTYKGRIE1IDQK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
W.B. Traxip-10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.4%; Score 124.5; DB 11; Length 329; 25.1%; Pred. No. 0.0011;
                                                                           14.9%; Score 197.5; DB 13; Length 357; 28.0%; Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
TISSOUPERTRONDEN,
PRIDALINE-99180614; PubMed-10079287;
de la Prente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
                                                                                              Pred. No. 1.3e-10;
41; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93; Indels
                                         274161DF83868C08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37345 MW; 43BB1AA5AF1989E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 SSI-ILTTCIPS-SGHSRHRYALIPIPLAVITTCIVLYMNGIL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 DSVTVQQPCTDTPSFHPRH--AVLPGGLAVLFLLILIPMLAFL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBirel 10, Created)
01-MAY-1999 (TrEMBirel 10, Last sequence update)
01-DEC-2001 (TrEMBirel 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   202 LITCIPS-SGHSRHRYALIPIPLAVITICIV----LYM 234
                                                                                                                                                                                                                                                                                                                                                                                                          196 LDGCSPTYGGYSSPKRSRAGLITAVVAPLPVGAGLIYM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenetics 49:249-255(1999),
BEBL. AFG 445, AMDO2273.1;
WDD: WAIL1336885, Cd84,
InterPro: IRR003600; Ig_like.
SRMRT; SWOOLIO, IG_Like: 1.
SQUUSNCE 329 AA. 37345 MH; 43BB
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2,
SEQUENCE 357 AA; 39930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 25.1%;
                                                                                              Best Local Similarity 28.09
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD84 leukocyte antigen.
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583 VKSNIVLYGSSSPPIILLEDQNKKDKQEIGDNTTSVIHTYELINNGPSDISSGTINIKW 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 LIMYSWDCPMEQCKRN-----STSIYFK--MENDLPQKIQCTLSNPLFN----- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                700 CVVFS - CSVDMLRANEXVTVSIESSLLLKTVLENDLDSEIRSEFEFKIDSYPYPINLGP 757
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                                                                                                                                                                                                                                                                                                                                                                        67 ENSEFARSSFKNRVYLDTVSG-SLTIYNLTSSDEDEYE------MESPNITDTMK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                             116 PELYVLESIPSPTLT-----CALTNGSIEVOCNIPBHYNSHRGLIMYSWDCP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 --LSVKADEPTPSITDFEIPPSNIRRIICSTSGG------FPEPH------LSWLEN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 VYGNVIFHVPSNVPLKEVLWKKOKDKVAELENSEPRAFSSFK--NRVYLDTVSGSLTIYN 94
                                                                                   13 VISVVCLLH-CFGFISCFSQQIYGVVYGNVTFHVPSNVPLKE-----VLWKKQKDKVAEL 66
                                                                                                                                                                      MEDIANE TROWN TO THE TROWN THE TOWN THE TROWN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 MEQCKRNSTSIYFKMENDLPQKIQCTLSNPL-FNTTSSILLTTCIPSSGHSR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 GEELMAINTIVSODPETEL-----YTVSSKLDFNWTTNHSF-MCLIKYGHLR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 833;
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21.0%; Pred. No. 0.17;
tive 55; Mismatches 102; Indels
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Stolidobranchia: Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 833 AA; 91785 NW; 735564C4BAD4B14A CRC64;
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01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
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SMART; SMO0191; INT_alpha; 4.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
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Pfam: PF01839; FG-GAP: 4.
Pfam: PF00357; integrin_A: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halocynthia roretzi (Sea squirt).
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Matches 51; Conserva
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09BPQ7;
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An Weiters W.F., America W.F.,
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Manayota, Metazoa; Chordata; Cranhata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercoptinecidae;
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF079519; AAC11555.1; *.
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288 AA; 33141 MW; E70BEA4006C7A609 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 -VNSNI-----SBEGVCNISLTCSIERAGMDVTYIWLSSODSTNTSHEGSVLST 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 BEVVGVEQBSINLSLEIPSNEEIKHIDMLFONNIAIVKPGKKGQPAVIMAVDPRYR---- 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 QQIYGVVYG--NVTFHVPSNVPLKEVLM------KKQKDKVAELENSEFRAFSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.9%; Score 105; DB 11; Length 285; 2.1%; Pred. No. 0.065; ve 29; Mismatches 74; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART, SMO0409; IG; 1.
SMART; SM00410; IG_LIKe; 1.
SEOUENCE 285 AA; 31764 MM; 338DB4A633A5C1B3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AELBNSEFRAFSSFKNRVY-LDTVSGSLTIYNLTSSDEDBYENESPN---ITDTMKFFLY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 VTWDTTDNKNFNMCCSDIYGFBSENFALSIKSAKLNDSGHYLLEITNQRGIVCTKNFQML 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 VLESLPSPTLTCALT --- NGS -- IEVOCMIPE --- - HYNSHRGLIMYS --- -- WDCPM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 IFDPVETPHLTVQGTLWANGTCQLSLSCFVPKDDNVSYALYRGSMLISNQRYGTHW---- 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kumaresan P.R., Stepp S.E., Bennett N., Kumar V., Mathew P.A.;
Nobeclar Coloning of transmembrane and Soluble forms of a novel rat
natural killer cell receptor related to ZBM.";
Immosphetics 51:306-313(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VLSVVCLLHCFGFISC--FSQQIYGVVYGNVTFHVPSNVPLKEVL--WKK-----QKDKV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LLSLFLLLRAHOGODCADSSEEVLGVSGRPVRLR-PSNIQAKHVSIEWKKTGHQQTPQI 65
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Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.0%; Score 105.5; DB 11; Length 311; Best Local Similarity 21.6%; Preci. No. 0.05; Matches 99; Indels 59; Matches 99; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 AA: 35300 NW: 5A527D22D2565772 CRC64:
                                                                                                                                                                                                                        01.077-2000 (TrEMBLrel. 15, Created)
01.077-2000 (TrEMBLrel. 15, Last sequence update)
01.017-2001 (TrEMBLrel. 17, Last annotation update)
NR cell receptor 284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 LPPMVSIGILVKFFHGAIDCFCVWNRKRKOSOS 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-20260988; Pubmed-10803843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01.JUN-2001 (TIENBLIE). 17, CR
01.JUN-2003 (TIENBLIE). 17, LM
01.JUN-2002 (TIENBLIE). 21, LM
2310026104RK protein.
CDZP10 OR 2310026104RK.
MUS MUSCHLUS (MOUSE).
                                                                                                                                                       PRELIMINARY:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 WVAGSDAGRALGVUCLL......MEDALHNHYTQKSLSLSPGK 347
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                                                                                                                                                                                                                                                                      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283224 seqs, 96134422 residues
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A MORE: this sequence has the Carlot parker, 97-Arg and sequence has the carlot parker, 97-Arg and 97
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Greeker, L. S. Tobhear, J. J. Senbiell, W. H. Labenbann, N. H. Stocker, L. S. Schouler, J. Stocker, J. Stocker,
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X. Intrachain disulfid
A:Reference number: A90565; NUID:71064027; PMID:4923144
                   Acresiones, 1310 cBLs.
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A-Modelings: 1.56, 747, 595-197, 10, 139-238, TP, 240, 747, 742-266, 70, 268-271, 70, 273-330
A-Modelings: 1.56, 747, 595-197, 70, 139-238, TP, 240, 747, 742-266, 77, 268-271, 70, 773-330
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A; Reference number: S33904
A; Accession: S36861
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A; Residues: 2-330 <HAR>
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ArAccession: mycloma protein &ide
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                                                                                             121 DKTHICPPCPAPELLGGPSVFLFPPKPKDTLAISRIPEVICVVDVSHEDPEVKFNWYUD 180
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              A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
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                                                                                                                260 EKTISKAKGOPREPOVYTLPPSREBYTKNOVSLTCIVKGFYPSDIAVERESNGOPENYK 319
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A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contenters: annotation; Sa, disulfide bonds
C:Genetics:
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8; Mismatches 6
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B; Mismatches
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A. Arbecession 1999; protein
A. Arbecession 12-97 office
A. Arbect the hinge region in quamma-3 chains is about four times as long as in other quamma (Late segment (12-28))
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A Mediature 195-155, FBT, 178-256.228-289 GMOD.
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No. 1.6e-72;
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Gaps

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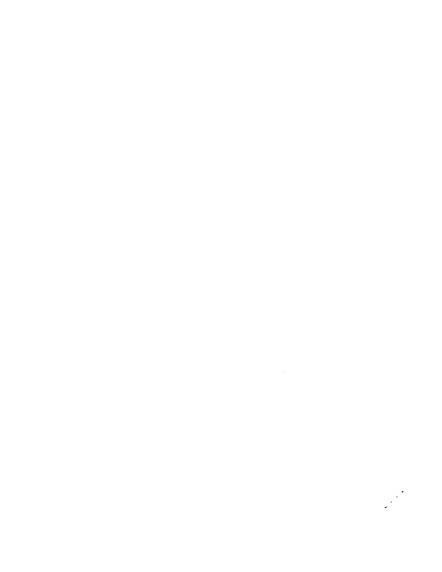
Best Local Similarity 58.8%, Pred. No. 2e-57; Indels 41; Gaps 7; Msches 181; Conservative 37; Mismatches 49; Indels 41; Gaps 7;	0	Oy 340 SEESCHOR 847 Db 331 SESCHOR 338 MESULT	C.Sepetas 3.8 accord demandia (Confidentia P. 18) C.Sepetas 3.8 accord demandia (Confidentia P. 18) C.Sepetas 3.8 accord demandia (Confidentia P. 18) C.Sepetas 3.7 acquared_available (Confidentia) C.Sepetas 3.7 acquared_available C.Sepetas 3.7 ac	C.Schwettenly, Immunoplobalia C. region, immunoplobalian homology F. Sil-Sil/Comail: Immunoplobalian homology 47849-71547 Guerry March (1847) Score (1847) Score (1865) Sup 2. Length 277; Buerch (Lond.) Similarity 71.53; Pred. Rob. 2.77-25; Inchial F. 77; Buerches (1867) Conservative 23; Maraches 21, Inchial F. 77; Gape 4, Robert (Lond.) Similarity 71.53; Pred. Rob. 2.77-25; Inchial F. 77; Gape 4, Robert (Lond.) Similarity 71.54; Pred. Rob. 2.77-25; Inchial F. 77; Gape 4, Robert (Lond.) Similarity 71.54; Cape 4, Robert (Lond	QP 175 PRINCIPORUMANE PREDIOTORISTICAL VILLIONICALE EX 234 DD 101 SERVICOPRUMANE PREDIOTORISTICAL VILLIONICALE VILLIONICAL EX 234 DD 101 SERVICOPRUMA PREDIOTORISTICAL VILLIONICAL EX 122 QP 231 TESAKADORISTICATORISTICANO/SETTI
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Tue Jan 28 09:45:23 2003

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A PRILES: Privacy structure of the C-#2 homology resis of ron guitnes pig 1962 antibodie A Ancesseo unmber, 20084; will'n's 1964 antibodie A Ancesseo unmber, 20084; will'n's 1964 antibodie A Ancesseo unmber, 20084; will'n's 1964 antibodie A Ancesseo and 20084; will'n's 1964 antibodie A ANTIES: Interface and 20084; will'n's 1964 antibodie A ANTIES: The Privace and 20085; will'n's 1964 antibodie A ANTIES: The Privace and 20085; will'n's 1964 antibodie A ANTIES: The Privace and 20085; will'n's 1964 and 20084; will'n's 1964 and 20085; will'n's 20085; will not 2
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48.18; Score 892; DB 1; Length 329;
66.64; Pred. No. 3.66-56; Dest Local Similarity 33; Mismatches 17; Conservative 33; Mismatches 77; Indels 38;
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Job time : 19.0184 secs
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CSPECION CANADA CONTROL WILLIAM PROPERTY OF THE PROPERTY OF 
                             C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 NITDTMKFFLYVDKTHTCPPCPAPELLGGPSVFLFPPKPXDTLMISRTPEVTCVVVDVSH 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 PAPIEKTISKAKGOPREDOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO-- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 PENNYKITPPVLDSDGSFFLYSKLIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 PENTYRTTPPOODUDGTFTLYSKLAVDKARMDHGDKFECAVMHEALHNHYTOKSISKTOG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: U03778; NID: q433121; PIDN: AAA52216.1; PID: q433122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 27; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
48.28; Score 894.5; DB 2; Longth 329;
Besst Local Similarity 8.88; Pred No. 2.46-56
Matches 177; Conservative 37; Mismatches 60; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Gene: 1961
C.Superfamily: immunoglobulin C region; immunoglobulin homology
Fil35-207/Domain: immunoglobulin homology <1805
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A; Residues: 69-133;312-329 <TUR>
R; Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-328 <KAC>
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		28	405	30.3	77	-	US-07-940-861-5	
	GenCore version 5.1.3	59	402	30.3	77	-	US-08-459-512-5	
	Copyright (c) 1993 - 2003 Compugen Ltd.	30	402	30.3	77	~	JS-08-459-657-5	
		31	402	30.3	77	c	JS-08-460-132-5	
		32	402	30.3	77	'n	PCT-US92-02050-5	
OM protein - pro	OM protein - protein search, using aw model	33	281	21.2	318	9	5223394-11	
		34	260	19.6	20	-	JS-07-940-861-2	
Run on:	January 28, 2003, 08:38:45 ; Search time 11,3065 Seconds	35	260	19.6	20	-	JS-08-459-512-2	
	(without alignments)	36	260	19.6	20	~	35-08-459-657-2	
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		38	260		20	s	PCT-US92-02050-2	
Title.	IIS-09-730-465-2	39	256.5		131	_	JS-08-328-152A-1	
Perfect score:	1326	40	200	15.1	38	ø	5185441-1	
Sequence:	1 MVAGSDAGRALGVLSVVCLLVLYMNGILKCDRKPDRTNSN 250	41	165	12.4	35	-	US-07-940-861-33	
		43	165	12.4	32	_	JS-08-459-512-33	
Scoring table:	BLOSIM62	43	165	12.4	32	2	JS-08-459-657-33	
	Gapop 10.0 . Gapext 0.5	44	165	12.4	32	~	US-08-460-132-33	
		45	165	12.4	32	'n	PCT-US92-02050-33	

sequence 5, App11
sequence 5, App11
sequence 5, App1
sequence 2, App1
sequence 3, App1

262574 seqs, 29422922 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Fotal number of hits satisfying chosen parameters:

ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Database :

Fred. No. 1s the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Match Length DB	8	OI.	Description	
-	1326	100.0	250	-	US-07-940-861-10	Sequence 10, Appl	
2	1326	100.0	250	٦	US-08-459-512-10	Sequence 10, Appl	
6	1326	100.0	250	2	US-08-459-657-10	Sequence 10, Appl	
4	1326	100.0	250	2	US-08-460-132-10	_	
8	1326	100.0	250	7	US-08-466-465-2	**	
9	1326	100.0	250	2	PCT-US92-02050-10	_	
7	1326	100.0	250	9	5223394-1		
89	1307,5	98'6	251	9	5185441-38	Patent No. 5185441	
6	1250	94.3	240	-	US-07-940-861-12		
10	1250	94.3	240	Н	US-08-459-512-12	12,	
11	1250	94.3	240	2	US-08-459-657-12		
12	1250	94.3	240	2	US-08-460-132-12	Sequence 12, App1	
13	1250	94.3	240	4	US-08-466-465-4	Sequence 4, Appli	
14	1250	94.3	240	ŝ	PCT-US92-02050-12	Sequence 12, Appl	
15	1250	94.3	240	9	5185441-36	Patent No. 5185441	
16	1250	94.3	240	ø	5223394-4	Patent No. 5223394	
17	1250	94.3	240	9	5223394-6	Patent No. 5223394	
18	1179	88.9	222	г	US-08-328-152A-8	Sequence 8, Appli	
19	647	48.8	134	٦	US-08-328-152A-13	23	
20	630	47.5	347	H	US-07-940-861-43	43	
21	630	47.5	347	-	US-08-459-512-43	43	
22	630	47.5	347	a	US-08-459-657-43	43	
23	630	47.5	347	~	US-08-460-132-43	43,	
24	630	47.5	347	*	US-08-466-465-8	Sequence 8, Appli	
25	630	47.5	347	S	pcr-us92-02050-43	-	
36		35.6	225	н	US-08-328-152A-31	Sequence 31, Appl	
27	447.5	33.7	199	н	US-08-328-152A-36		

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61 DKVAELENSEFRAFSSFKNRVYLDTVSGSLTIXNLFSSDEDEYEMESPNITDTMKFFLTV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LESLESPILICALINGSIEVOCATPERYNSHBGLINGSSADCPABOCKRASTSIYFKAEND 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 DPOKIOCTLSNPLFNTTSSILLTTCIPSSGHSRHRYALIPIPLAVITTCIVLYMNGILKC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1326; DB 1; Length 250; 100.0%; Pred. No. 1.7e-126; Live 0; Mismatches 0; Indels 0
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COMPUTER: Floppy disk
COMPUTER: IR NF COMPALIAN
OPERATING SYSTEM: PC-005/NS-008
SOFTWARE Patent PATENT PATENT PATENT PATENT NOTICATION DAYS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-1995
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ELING DATE: 12-NRR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-NAR-1991
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/770.967
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SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
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Matches 250; Conservative
                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-512-10
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CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/459,512
FILMS DATE: 02-UN-1995
CLASSIFICATION: 514
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RICHARD BATA.
REPLICATION BATA.
PCT/US92/02050
FILING DATE: US. TARK-195
PELLOR BATE: US. 07/667,971
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5728677
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IMPORMATION FOR SEQ ID NO: 10:
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.0
Matches 250; Conservative
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: MOLECULE TYPE: protein
US-07-940-861-10
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61 DKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDIMKFPLYV 120
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TITLE OF INVENTION: WEELDED OF PROPPLIANS OF Treatment of Antigen
TITLE OF INVENTION: Presenting CA31 Dirthen Skin Conditions Using
TITLE OF INVENTION: Inhibitors of the CD2/LRA-3 Interaction of
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
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FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/466,465
FILLING DATE:
REFERENCE/DOCKET NUMBER: BISICIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/08466465
; Patent No. 6162432
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APPLICANT: Wallner, Barbara P.
                                                                                                                                                            NAME: HALEY, James F., Jr. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
Matches 250; Conservative
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US-08-460-132-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1326; DB 2; Length 250; 100.0%; Pred. No. 1.7e-126; Live 0; Mismatches 0; Indels 0.
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APPLICANT: MILEMEN, BERNA, INC.
APPLICANT: MILEMEN, BERNA, BERNA, BORNER, BORNER, BORNER, BORNER, BERNARD, BORNER, BORNER, BERNARD, AND TITLE OF INVENTIONS: OF WASCULAND AND AND SEC
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
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FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: US/08/460,132 FILING DATE: 02-JUN-1995 CLASSIFICATION: 424
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; Sequence 10, Application US/08460132
; Patent No. 5928643
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IBM PC compatible
                  TELEPAX: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 10:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
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Matches 250; Conservative
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FILING DATE: 21-OCT:
APPLICATION NUMBER:
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RY: U.S.A.
10022-6250
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61 DKVARLENSERRESSFKSSFKNRVYLDTVSGSLTIYNLTSSBEDEYENESPNITDTMKFFLJV 120
61 DKVARLENSERRESSFKRSSFKNRVYLDTVSGSLTIYNLTSSBEDEYENESPNITDTMKFLJV 120
62 DKVARLENSERRESSFKRSSFKNRVYLDTVSGSLTIYNLTSSBEDEYENESPNITDTMKFLJV 120
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100.0%; Pred. No. 1.7e-126;
tive 0; Mismatches 0; Indels 0;
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APPLICANT, MALIANE, BARBARD
TITLE OF INVENTIONS, RECOMBINANT DAM, MOLECULE COMPRISING
LIMPROCITE PROFILE DATE OF ANTIONAL SECULE DATE OF ANTIONAL SECULE STATES SERVINGEN STATES SERVINGEN SECULES SERVINGEN SECULES.

INTERPRETATION SECURES. 12.

**INTERPRETATION SECURES.**

**INTERPRET
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APPLICATION NUMBER: US/07/335,688
FILING DATE: 10-APR-1989
          US 07/667,971
                                                                                                                                                                  APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-0CT-1991
APPLICATION NUMBER: US 07.
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                         ATTORNET/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
pcr-us92-02050-10
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Best Local Similarity
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181 LPOKIOCTLSNPLFNTTSSIILFTTCIPSSGHSRRRYALIPIPLAVITTCIVLYMNGILKC 240
181 LPOKIOCTLSNPLFNTTSSIILFTTCIPSSGHSRRRYALIPIPLAVITTCIVLYMNGILKC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%: Score 1326; DB 4; Length 250; DB 4st Local 100.0%; Pred. No. 1.7e-150 NB Matches 750; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAPRICONNY: NALLONG, NAPAGONE NAPAGONE NAPAGONE NALLONG; NALLONG SHARING SHARING SHARING NAPAGONE NAPAGONE NOSA, NANGHER D. SPENDING DOMIN OF LYMPHOCYTE NAPATION CO-SPENDING NASOCIATED NATIORN SHARING OF RECOMMENCE NAPAGONE NAPA
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WEDUN TYPE: Flopp disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFARE: PS-STEM: Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 19920312
APPLICATION NUMBER: US 07/862,022 PELINK DATE: 12-APR-1992 PRIOR APPLICATION NUMBER: US 07/770,969 FILING DATE: 07-00T-1991 ATTORNEY-ARRY INCORMATION:
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US-08-466-465-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLASSIFICATION: 435
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MEDIUM TIPE: Floppy disk computer: MEN Computer: MEN Computer SCHWART STATE MEN COMPUTER: 10. Version 11.25 SCHWART STATE MEN COMPUTER: 10. Version 11.25 CURRENT MEN COMPUTER: 1957/940.861 CLEEP MEN (21.1921/940.861 FROM APPLICATION NEW MEN. 1957/940.861 MEN COMPUTER: 10.1937/940.961	TO THE STATE OF TH	IDENTIFY AS Desired acids	GUNTEHUSENDIKEUHKK GUNTEHUSENDIKEUHKK SDEDEYEMESPULTDIMKFEL SDEDEYEMESPULTDIMKFEL SDEDEYEMESPULTDIMKFEL	07 121_LEGE_PERTOAL/REGEOVED_FERVENGENCENESSESTERMED 180	RESULT 10 100 4-59-512.12 Sequence 112.08 placation 03/08459512 Sequence 112.08 placation 03/08459512 SERREAL, 19000000000000000000000000000000000000
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61 DKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLYV 120
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                                                                                                                                                                                                                                                                                                                                                                         CLASSIPICATION: 474
CLASSIPICATION 1974
APPLICATION NUMBER: PCT/US92/02050
ELING DATE: 12-687-1992
APPLICATION NUMBER: US-057667,971
ELING DATE: 12-688-1991
PRIOR APPLICATION NUMBER: US-011
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FILING DATE: 07-OCT-1991
NAMP: .....
                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 5928643
GENERAL INFORMATION:
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REGISTRATION NUMBER: 27,794
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STREET: 875 Third Avenue
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MOLECULE TYPE: protein
US-08-459-657-12
COMPUTER READABLE FORM:
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                                                                                                                                        OPERATING SYSTEM:
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10022-6250
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STATE: New York
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-460-132-12
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Pred. No. 8.3e-119;
1; Mismatches 0; Indels
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                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/459,512
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
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Patent No. 5914111
GENERAL INFORMATION:
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                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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Best Local Similarity 99.6%
Matches 236; Conservative
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US-08-459-512-12
COMPUTER READABLE FORM
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COUNTRY: U.S.A.
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COMPUTER READABLE FORM

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61 DKVAELENSEPRAPSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLYV 120
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Pred. No. 8.3e-119;
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                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Myers, Louis (PLM)
REGISTRATION WHOMER: 35,965
REPERRNED/DOCKET NUMBER: 86-111CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/770,969
FILING DATE: 07-0CT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/466,465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/862,022
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; GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
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875 Third Avenue
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SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ne
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Best Local Similarity
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10022-6250
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121 LESLE/SPTLTCALTNGSIEVQCMIPEHYNSHRGLIMYSWDCPMEQCKRNSTSIYFKWEND 180
121 LESLE/SPTLTCALTNGSIEVQCMIPEHYNSHRGLIMYSWDCPMEQCKRNSTSIYFKWEND 180
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Pred. No. 8.3e-119;
1; Migmatches 0; Indels (
MEDIUM PEER, EPPOPU disk
COMESTER: 118 PC COMPACILIA
OPERATING SYSTEM: PC -1005/48-505
SOFTWARE: Patentin Release 11.0, Version 11.25
CURRENT APPLICATION DATA.aces 11.0, Version 11.25
FILMEN DATE: 02-109-1995
FILME DATE: 02-109-1995
GLASSIFICATION: 424
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APPLICATION NORTH: 07/940.861

APPLICATION NUMBER: 07/940.861

APLICATION NUMBER: 07/0592

APLICATION NUMBER: 07/0592/02050

FILME DAYE: 12-MAR-1992
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60 State Street, Suite 510
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PRILIKE DATE: 05 07770,967
FILINE DATE: 07-005-1991
NAME: HALEY, James P. 1,794
REGISTRATION NUMBER: 27,734
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
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Patent No. 6162432
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TELEPAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ. ID NO: 12:
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Best Local Similarity 99.6%;
Matches 236; Conservative
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LENGTH: 240 amino acids
TYPE: amino acid
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US-08-460-132-12
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61 DKVAELENSBERAFSSFKNRVYLDTVSGSLTIYNLTSSDBDEYRMESPNITDTMKFFLYV 120
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                1 MVAGSDAGRALGVLSVVCLLHCFGFISCFSQQIYGVVYGNVTFHVPSNVPLKEVLWKKQK 60
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Job time: 13:3065 secs
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1918-01 NO 195441
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APPLICARY WALLARE BARBARA P.:HESSIONS, CATHERINE
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COMPUTER PROCHABLE PROCHABLE
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Pred. No. 8.3e-119;
1; Mismatches 0;
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FILING DATE: 19920312
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 26-AUG-1988
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TELEX: 14-8167
TELEX: 14-816
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REGISTRATION NUMBER: 27,794
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 99.6%;
Matches 236; Conservative
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FUNCHER OF SEQUENCES: 41
CURRENT APPLICATION DATA:
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PCT-US92-02050-12
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Copyright (c) 155 - 205 Copyright (c) 156 - 205 Copyright (c) 156 Copyri	Prost-processing Marie and School Marie and S	Pred No. is the number of regard predicted by the character of the regard between the content of the chair growed of the chair growed of the chair growed distribution. **Content than or equal to the cont of the regard between the chair growed of the chair growed distribution. **Description** **Part of the chair growed distribution of the chair growed of the cha

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TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
Presenting Cell Driven Skin Conditions Using
Inhibitors of the CD2/LEN-3 Interaction
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Pred. No. 1.8e-105;
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STREET: 60 State Street, Suite 510
CITY: Boston
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Patent No. US20020009446A1
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Patent No. US20020009449A1
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TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
TITLE OF INVENTION: Method Of Prophylaxis or Treatment of Antigen
Thisticos of the CO2/MEN-3 interaction Using
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MEDLIM TPPE: FLORPY disk
COMPUTER: IIBM FO-COMPALINE
OPERATING SYSTEM FO-TOS/98-DOS
SOFTMER: Patentin Stelesse 11.0, Version 11.25
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Matches 250; Conservative 0; Mismarch.
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FILING NNE: 06-00-1992
APPLICATION NUMBER: 05 07/062,022
APPLICATION NUMBER: 05 07/770,059
APPLICATION NUMBER: 05 07/770,059
APPLICATION NUMBER: 07 07/770,059
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STREET: 60 State Street, Suite 510
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REGISTATION WINBER: 35,965
REPERENCE/DOCKET NUMBER: BGP-111CP
TELECOMMUNICATION INFORMATION:
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FILING DATE: 05-Dec-2000
PRIOR APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-730-465-2
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TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-730-465-2; Sequence 2, Application US/09730465; Patent No. US20020009449A1
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CORRESPONDENCE ADDRESS:
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52.8%; Pred. No. 2.1e-49;
Live 22; Mismatches 41; Indels
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Similarity 52.8%; Pred. No. 2.1e-49;
51; Conservative 22; Mismatches 41;
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; Sequence 8, Application US/09796033
; Patent No. US20020009446A1
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Matches 151; Conservative
                                                                                                                                                                                                                                                                                         Conservative
                                                                                     ORGANISM: Homo sapiens
US-10-091-236-17
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LENGTH: 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LPQKIQCTLSNPLPNTYSSILLTTCIPSSGHSRHRYALIPIPLAVITTCIVLYMNGN 237
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                                  ZIP: OXIGO-1878
ZORWITER REALABLE FORM: THE FLORE OR THE COMMUNICATION OF THE FLORE FLORE OF THE FLORE FLORE
                                                                                                                                                                                                                                                                                                                                   NAME: Myers, Tours (PLM)
RANGESTRATION NUMBER: 35,965
REPRENCE/OCKET NUMBER: BEP-111CP
TELEPHONE: (617)22-7400
TELEPHONE: (617)22-7400
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-730-465-4
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PRIOR PILIMS DATE: 2001-03-02
PRIOR PILIMS DATE: 2001-03-02
PRIOR PILIMS DATE: 2001-08-31
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Patent No. US20020168360A1
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SEQUENCE CHARACTERISTICS:
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Matches 236; Conservative
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15 IMYSW-----DCPMBOCKRNST----SIYFKMENDL--POKIOCILSN----P 192
                                                                                       I73 VKFNWYVDGVEVHNAKŢKPREE-QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 YLDTVSGSLTIYNLTSSDEDEYEM----ESPNITDTMKFFLYVLESLPSP----- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 -----GTLKIKHLKTDDQDIYKVSIYDTKGKNVLEKI-FDLKIQERVSKPKISWTCINT 142
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TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Parelling CAI Driven Six loodstions Saing
Thilbitors of the 002/LRF-3 interestion
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23.0%; Fred. NO. 0.0049;
18.1ve 42; Mismatches 76; Indels 79; Gaps
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TITLE OF INVESTICION FORTION FORTION FOR ADDITION FOR THE SHORT ADDITION FOR
                                                                                                                                                                                        193 LPNTTSSILLTTCIPSSGHSRHR--YALIP-----IPLAVITCIV 231
                                                                                                                                                                                                                                                                               232 IEKTISK-----AKGOPREPONYTLPPSRDELTKNOVSLTCLV 269
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Patent No. US2002009446A1
GENERAL INFORMATION:
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Patent No. US20020009449Al
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CORRESPONDENCE ADDRESS:
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Best Local Similarity 23.0%
Matches 59; Conservative
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US-09-796-033-6
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LENGTH: 351
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61 DKVAELENSEFRAFSSFKHRYLDTVSGSLTITNLTSSDEDEYEMESPHITDTMKFFLYV 120
61 DKVAELMSSFRAFSFRAFSFKHYLDTVSGSLTITNLTSSDEDEYEMESPHITDTMKFFLYV 120
62 DKVAELMSFRAFSFRAFSFKHYLDTVSGSLTITNLTSSDEDEYEMESPHITDTMKFFLYV 120
173 VKFNWYVDGVEVHNAKTKPREE-QYNSTYRVUSVLTVLHQDMLNGKEYKCKVSNKALPAP 23I
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WHOTHER RELABATE FORM:
WHOTHER RELABATE FORM:
OFFERTING STEPRE, RC. TOTAL STEPRE
                                                                                                                                       193 LFNTTSSIILTTCIPSSGHSRHR--YALIP-----IPLAVITTCIV 231
                                                                                                                                                                                                                                         232 IEKTISK-----AKGOPREPOVYTLPPSRDEL/TKNOVSLTCLV 269
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CORRESPONDENCE ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
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FILING DATE: 06-OCT-1992
APPLICATION NUMBER: US 07/862.022
FILING DATE: 12-APR-1992
APPLICATION NUMBER: 03 07/770,969
APPLICATION NUMBER: 07-770,969
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-5400
TELERAX: (617)227-5941
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REGISTRATION NUMBER: 35,965
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APPLICANT: Wallner, Barbara P.
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Patent No. US20020009449Al
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TYPE: amino acid
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COUNTRY: USA
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STREET: 60 State Street, Suite 510

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APPLICANT: Chapit, Seven 1, Seven 2, Seven 2, Seven 3, Seven 4, Seven 4, Seven 5, Se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 GSVTIRCPYNPKRSDSHLQLYLWEGSQTRHLLVDSGEGLVQKDYTGRLALFEEPGNCTFS 422
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 P-BHYNSHRGLIMYSWDCPMBOCKRNSTSIYFKMENDLPQKIQCTLSNPLPNTTSSIILT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 PCKYFSSEK----YW-----CKWNDHGC-----BDLPTKL--SSSGDLVKCNNNLVLT 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 GNVTFHVP----SNVPLKEVLWKKQKDKVAELENSEFRAFSSFKNRVYLDTVSG----S 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 GNVTEHVP----SNVPLKEVLWKKOKDKVAELENSEFRAFSSFKNRVYLDTVSG----8
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                                                                                                                                                                                                                                                                                                                                                                            79: Indels 49:
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                                                                                                                                                                                                                                                                                               Query Match 8.0%; Score 105.5; DB 9; Length 773; Best Local Similarity 22.0%; Pred No. 0.11; 0.11; Matches 49; Indels 49; Matches 47; Conservative 39; Manatches 79; Indels 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | | | | | 523 LILDSVSEDDEGMYWCGAKDGHEFEEVAAVRVEL 556
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PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 26
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7.5-09-818-247-6
7.5-09-ence 6, Application US/09818247
7.5-09-ence 10. US20020102657A1
                                                                                                                                                                          ; ORGANISM: Oryctolagus cuniculus
US-09-982-107-2
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NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
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                                                                             SEO ID NO 2
                                                                                                            LENGTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 -----GTLKIKHLKTDDQDIYKVSIYDTKGKNVLEKI-FDLKIQERVSKPKISWTCINT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 YLDTVSGSLTIYNLTSSDEDEYEM----ESPNITDTMKFFLYVLESLPSP----- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 TLTCALINGSIEVOCHIPE-----HYNSHRGLIMYSWDCPMEDCKRNSTSIYFKMEN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 TLTCEVMNGT-----TTS-----179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 DLPQKIQCTLSNPLFNTTSSIILTTCIPSSGHSRHRYALIPI-----PLAVITTCIVLYM 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 -LSAKFKCTAGNKV-SKESSVEPVSC-PEKG--LDIYLIIGICGGGSLIMVFVALLVFYI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76; Indels 79; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 ETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDKKKIAQFRKEKETFKEKDTYKLFKN-- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 QIYGVVYGNVTPHVPS---NVPLKEVLWKKQKD--KVAEL--ENSEFR---AFSSFKNRV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MOTHODS FOR PRODUCING IMMUNOCLOBULING CONTAINING TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

8.7%, Score 115.5; DB 10, Length 351, PB st Local Similarity 23.0%; Pred. No. 0.0049, Matches 59, Conservative 42; Mismatches 76; Indels 79, Matches 59, Conservative 42; Mismatches 76; Indels 79,
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US92/08755
FILING DATE: 06-027-1992
APPLICATION NUMBER: US 07/862,022
APPLICATION NUMBER: US 07/862,022
APPLICATION NUMBER: US 07/70,969
FILING DATE: 07-027-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-111CP
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/730,465
FILING DATE: 05-Dec-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                          COMPUTER REACHELE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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CURRENT FILING DATE: 2001-10-16
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TELEFRA: (617)27-7401
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Patent No. US20020159958A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 351 amino acids
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                                                                     STATE: Massachusetts
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APPLICANT: HIATT, ANDREW C.
APPLICANT: HEIN, MICH B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 NGILKCDRKPDRTNSN 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                            COUNTRY: USA
ZIP: 02109-1875
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                                              CITY: Boston
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481 POKYFSSEK-----YW-----CKWNDHGC-----BDLPTKL--SSSGDLVKCNNNLYLT 522

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APPLICANT: Zhang, Zemin TTILE OF INVENTION: Zhang, Zecreted and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Secreted Encoding the Same
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                                                                                                                                                                                                  Sequence 253, Application US/09992598
Patent No. US20020160384A1
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watanabe, Colin K.
Williams, P. Mickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                        Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney, Austin L.
Kliavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood, William I.
                                                                                                                                                                                                                                                                                  APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fong, Sherman
                                                                                                                                                                                                                                                           GRNERAL INFORMATION -
242 RKPD 245
                                                   231 ROEE 234
                                                                                                                                         RESULT 13
US-09-992-598-253
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APPLICANT:
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Best Local Similarity 21.7%; Pred. No. 0.83; Matches 35; Conservative 42; Mismatches 107; Indels 42; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 GYSLKLSKLKKNDSGIYYVGIYSSSLQOPS---TOBYVLHVYEHLSKPKVTMGLQSNKNG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 SIEVQ---CMIPEHYNSHRGLIMYSWDCPMEQCKRNSTSIYFKM-----ENDLPQKIQCT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TCVTNLTCCM--EHGEED---VIYTWKALGOAANESHNGSILPISWRWGESDM--TFICV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 LSNPLFNTTSSIILTTCI-----PSSGHSRHRYALIPIPLAVITTCIVLYMNGILKCD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 ARNPVSRNPSSPILARRICEGGAADDDDSSMVLLCLLLVPLLLSLFVLGLFLM---FLKRE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 QQIYGVVYGNVTFHVPSNV-PLKEVLWKKOKDKVABLE-NSEFRAFSSFKNRVYLDTVSG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 KELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIVTQNRNRERVDFPDG 63
                                                                                                                                                                                                                                                                                                         APPLICAM: Michadoust, Mehran
TITLE OF INMENTION: NOVEL MF-7 PROPER AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USSS THERROP
UNDER OF SOURCESS: CORRESPONDENCE ALD SEESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
                      204 T-----CIPSSGHSRHRYALIPIPL 223
                                                                                523 L#LDSVSEDDRGWWGCAKDGHEFREVAAVRVEL 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: LAHIVE & COCKFIELD, LLP
28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: MNI-048CP
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APPLICATION NUMBER: 09/261,759
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                                                                                                                                                                                                                         Sequence 4, Application US/09732524
Patent No. US20020004193A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
TELEPHONE: (617)227-7400
TELEPAT: (617)724-4214
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: 11---
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FILING DATE: 1998-JUN-25
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US.
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
: USA
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                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boston
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                                                                                                                                                                     RESULT 12
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FILING DATE: 1988-06-17
APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/087759
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FILING DATE: 1998-06-18
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87 GYSLKLSKLKKNDSGIYYVGIYSSSLQQPS ---TQEYVLHVYBHLSKPKVTMGLQSNKNG 143
                                                            137 SIEVQ---CMIPEHYNSHRGLIMYSWDCPNEQCKRNSTSIYFKM----ENDLPQKIQCT 188
                                                                                                    189 LSNPLFNTTSSIILTTCI-----PSSGHSRHRYALIPIPLAVITTCIVLYMNGILKCD 241
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Patent No. US2002017154A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi. Avi J.
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APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleone
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Baker, Kevin P.
Botstein, David
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        21.7%; Pred. No. 0.91;
tive 42; Mismatches 107; Indels 42; Gaps
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                                                                                                                                                                                                                                                                                                                                                                            87 GYSLKLSKLKKNDSGIYYVGIYSSSLQQPS---TQEYVLHVEHLSKPKVTMGLQSNKNG 143
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                                                                                                                                                                                                                                       27 KELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIVTQNRNRERVDFPDG 86
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NUMBER OF SEQ ID NOS: 170
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Publication No. US20020182638Al
GENERAL INFORMATION:
        Best Local Similarity 21.7%
Matches 53; Conservative
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US-10-063-547-46
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Search completed: January 28, 2003, 08:53:00 Job time: 83.077 secs . Db 254 RQEE 257

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GenCore version 5.1.3 Copyrisht (c) 1993 - 2003 Composen Ltd.	OM protein - protein search, using av model Run on: January 28, 2003, 08:38.55; Search time 37,7805 Seconds (officer dispused)	Title: US-09-710-465-8 ERF Cot sort: 19 WASSDARMANISWULL	Scoring table: BLOSHN62 Gapop 10.0, Gapext 0.5	Searched: 908470 seqs, 133250620 residues	Total number of hits satisfying chosen parameters: 908470 Minimum DB seq length: 0	s inc	Databae : A.comesog 101002; 21 KRISSZ-godat Krýpensegy (pantesep; emb.). AM 180 DRT: 22 KRISSZ-godat Krýpensegy (pantesep; emb.). AM 181 DRT: 23 KRISSZ-godat Krýpensegy (pantesep; emb.). AM 181 DRT: 24 KRISSZ-godat Krýpensegy (pantesep; emb.). AM 181 DRT: 25 KRISSZ-godat Krýpens		110 / STIDSZ/ Quiglach/ Agrees/ Quenes-op-pain/ AM/199 / JMT: • 111 / STIDSZ/ Quiglach/ Agrees/ Quenes-op-pain/ AM/199 / JMT: • 112 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 113 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 114 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 115 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 116 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 117 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 118 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 119 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 119 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 110 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 111 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 112 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 113 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 114 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 115 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 116 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 117 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 118 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 119 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 110 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 110 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 111 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 112 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 113 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 114 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 115 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 116 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 117 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 117 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 117 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 117 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 117 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 117 / STIDSZ/ Special En/ Quenes-op-pain/ AM/199 / JMT: • 117				Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the rotal score distribution	SUMMARIES	Result Ouery No. Score Match Length DB ID Description	1856 100.0 347	1856 100.0 347 23 AAU76228 1834 98.8 347 14 AAR34224	1255.5 67.6 633 1255 67.6 477

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Selective modulation of memory effector T lymphocytes by administration of a CD2 binding agent which inhibits the CD2.THY-3 interaction useful for treating conditions such as inflammatory boyel diseases, psociation
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       rheumatoid arthritis; multiple sclerosis; atopic dermatitis; uveitis; infiammatory bowel disease; crohn's desesse; ulcerative colitis; cuteneous 7 cell lymphoma; inhibition; treatment;
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Pred. No. 2.1e-128;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 75-76; 76pp; English
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                                                                                                                                                                                                     Homo saptens.
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                                                                                                                                                                                                                                                                                                                                                                                                                 CD2-binding domain of lymphocyte function associated antigen-3 and DNA for diagnosing and treeting infilammation and auto: immune diseases, e.g. systemic lupus erythematosus and auto:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.0%; Score 1856; DB 13; Length 347; DB 50 be 13; Length 347; DB 50 be 100.0%; Pred. No. 2.1e-128 be 100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFA3; CD2; cell signalling; modulation: lymphocyte; T cell; memory effector T lymphocyte; psoriatic arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ž
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                                     91US-0667971
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                                     12-MAR-1991;
                                                                           07-0CT-1991;
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                                                                                                                                                Human, LRA3TIP; antipsoriatic; dermatological; antiinflammatory;
antiallergic; vasorropic; skin condition; T-cell adhesion molecule
Unphocyte function-associated antiqen-3; LRA-3; atopic dermatitis;
cuttaneous 7 cell lymphoma, fusion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prophylaxia or treatment of Skin conditions such as dermattiis, and pepcia areata, psoriasis, urticaria in mammala, by administering almabilitor of T-cell addesion molecula CD2/lymphocyte function-associated antigen-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1856; DB 22; Length 347; 100.0%; Pred. No. 2.1e-128; ive 0; Mismatches 0; Indels 0;
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              AAB61160 standard: Protein: 347 AA
                                                                                                                    Human LFA3TIP fusion protein.
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92WO-US08755
                                                                                    (first entry)
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                                                                                    30-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                     07-0CT-1991;
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06-0CT-1992;
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AAB61160
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61 DKVAELENSEPRAFSSFKHRVYLDTVSGSLTIVNLTSSDEDEYEMESPHITDTMKFFLVV 120
61 DKVAELENSEFRAFSSFKHRVYLDTVSGSLTIVNLTSSDEDEYEMESPHITDTMKFFLVY 120
61 DKVAELENSEFRAFSSFKHRVYLDVSGSLTIVNLTSSDEDESPHITDTMKFFLYY 120
                                                                                                                                                                   121 DKTHTCPPCPAPELLGGPSVFLFPPKPCTLKISRTPEVTCVVVDVSHEDPEVKFNWYVD 180
                                                                                                                                                                                                                                                     121 DKTHFCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 180
                                                                                                                                                                                                                                                                                                                                                                                  GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFA3/IgG fusion protein (LFA3TIP).
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Location/Qualifiers Mammalia. Peptide

"Mature LFA3TIP protein" 1..28 /note= "Signal peptide" /note=

92US-0862022 92WO-US08755 910S-0770969 95US-0466465 07-0CT-1991; 12-APR-1992; 16-JUN-1995;

Wallner BP, Cooper KD; WPI; 2002-179118/23 BIOJ) BIOGEN INC

Treating conditions characterised by increased T cell activation and above man antique presentation in the demis and epidemia, e.g. atopic deformatics, vitility each UV damage, by administering an inhibitor of the CD2/LFA-3 interaction N-PSDB; ABK15720.

Phis invention relates to a novel method for preventing or treating skin Example 3; Page 21-22; 32pp; English.

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61 DKVAELENSEFRAFSSFRNRVYLDTVSGSLSIYNLFSSDEDEYEMESPNITDTMKFFVYV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paralle (Aballe), amoding Pality I is deposited under Arcs 6879.
The fution protein comprises the asino testinal 32 amino acids of the fution protein comprises the asino testinal 32 amino acids of the fution of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion protein; chimeric protein; pharmacokinetic;
vascular permeability; IgG Fc region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1834; DB 14; Length 347;
Pred. No. 8.8e-127;
2; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                   Improving tolerance of transplanted allo:graft or xenograft tissue - using LFA-3 or CD-2 binding protein esp. for humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSFGK 347
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                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure: Page 58-59; 68pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ž
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Conservative
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                                                                                                                                                                                              APT: 1993-134134/16
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                                                                                                                                                                                                                            N-PSDB; AAQ40423.
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plasma leakage;
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Matches 343:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1856; DB 23; Length 347;
100.0%; Pred. No. 2.1e-128;
1ve 0; Mismatches 0; Indels 0;
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Tue Jan 28 09:45:18 2003
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Matches 347; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AA:
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the Pill receptor and the Fr Espino of 195. The specification calata
to smallted chimaric polyapida with improved pharmacolitatics. The
modified chimaric polyapida with proved pharmacolitatics. The
modified chimaric polyapida was preferably statistic proper of 112 prefit
control of 1950 and 195
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                                                                                                                                                                                                                                                                                                                        Nucleic acid molecule encoding mammalian phospholipid transfer protein.
                                                                                                                                                                                                                                                                                                                                                  and its fragments, useful for diagnosis, evaluation, and treatment of
diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 NCTARTELNVGI-DENWEYPSSKHOHKKLVNRDLKTQSGSEMKKFLST----LTIDGVTR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDEDEYEMESPNITDIMKFFLYV-----DKTHTCPPCPAPELLGGPSVFLFPPKPKD 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 HODWINGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 HODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 KGFYPSDIAVEMESNGOPENNYKTTPPVIDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              881 KGFYPSDIAVEMESNGOPENNYKTTPPVLOSDGSFPLYSKLTVDKSRMOGNVFSCSVMH 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 NVTEHVPSNVPLKEVLWK --KQKDKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cellular adhesion molecule; ACAM; nootropic; antiepileptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.1%; Score 1263.5; DB 22; Length 458; 78.0%; Pred. No. 9.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                            Yancopoulos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY94408 standard; Protein; 744 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 49; Fig 21; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 EALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 EALHNHYTOKSLSLSPGK 458
                                99HS-0138133
                                                                                                 (REGE-) REGENERON PHARM INC
                                                                                                                                                            Papadopoulos NJ. Davis S.
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                                                                                                                                                                                                                      WPT: 2001-071076/08
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                                                                                                                                                                                                                                                             N-PSDR: AAA91074
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                                08-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and disd chinearic polypopides are preferably Fit teceptor polypopides. That have been modified to improve their pharmacokinetic profile. The polypopides con be used to derroase or inhibit plasma leakage and/or vascular perseability in a mammal.
                                                                                                                                                                                                                      Nucleic acid molecule encoding mammallan phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the one expression and for producing model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a fusion protein of the invention between
the Pill receptor and the Pr cepton of igg. The specification relates
to modified chimeric polypoptides with improved pharmacokinetics. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 SDEDEYEMESPNITDIMKFFLYV----DKTHTCPPCPAPELLGGPSVFLFPPKPTLM 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 SDOGLYTCAASSGLMTKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKDFLM 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREBQYNSTYRVVSVLTVLHQD 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 15RPPEVICVVVDVSHEDPEVKENNYVDGVEVHNAKTKPREBOYNSTYRVVSVLTVLHDD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 WLNCKEYKOKYSNKALPADIEKTISKAKGOPREPOYTLPPSKDELTKNOVSLTCLVKGF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHEAL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 NCTARTELNVGI-DFNWEYPSSKHOHKKLVNRDLKTOSGSEMKKFLST----LTIDGVTR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.0 NVTEHVPSNVPLKEVLMK --KOKDKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WINGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1265; DB 22;
Pred. No. 7.7e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.
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                                                                 Yancopoulos GD:
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 49; Fig 24; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.28;
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(REGE-) REGENERON PHARM INC
                                                                 Davis S.
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Best Local Similarity 78.79
Matches 248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 HNHYTOKSLSESPGK 347
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                                                                                                                                  2001-071076/08
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                                                                 Papadopoulos NJ.
                                                                                                                                                                  N-PSDB: AAA91076
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The present sequence represents a synthetic Coloractic cliestic cliestic for which serves and beautiful coloractic cliestic cliestic cliestic state which serves and beautiful coloractic cliestic cliest
                                                                                                                                                                                                                                                                                                                                                                    CD20-specific receptor; CD-20 specific redirected T cell; leukemia; CD20-malignancy; non-Hodgkin's lymphoma; mycobablative chemochterapy; stem cell rescue; autofamune disease; lupus; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetically engineered CD20-specific redirected \pi cells useful for treating a CD20+ analignancy, such as non-Hodgkin's lymphoma or CD20+ redecting or cD00-specific or chronic lowkemia, and autofimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "signal peptide from murine 786.66 antibody
kappa light chain"
                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a CD-20 specific chimeric receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21..126 /note= "anti-CD20 variable regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "CD4 transmembrane region"
                          709 VDKSRWOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "hlnge region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .266
--- "GS18 llnker"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "CH3 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "zeta chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jocation/Qualiflers
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                                                                                                                                                             AAX84965 standard; Protein; 633
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                                                                                                                                                                                                                                                                      21-AUG-2000 (first entry)
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283..392
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522..633
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                                                                                                        RESULT 9
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                                                                                                                                   AAY84965
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                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding ACAM, a human cellular adhesion molecule, useful for disprosing, preventing and treating diseases associated with ACAM expression and activity, e.g. epilepsy and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 GLVMGSSVTVSCKVPSVYPLDRLEIELKGETI-LENIEFLEDTDMKSLENKSDEMTFIP 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 TVSG---SLTIYNLTSSDEDEYEMESPNITDTMKFFLYV------DKTHTCPPCPA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 PELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWXVDGVEVHNAKTKP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 PELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNWYVDGVEVHNAKTKP 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 REBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 REEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALDAPIEKTISKAKGOPREDOVYTL 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 PPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 GVVYGN----VTFHVPSNVPLKEVLWKKQKDKVAELENSEFRAFSSFKN-----RVYLD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   649 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESKGQPENNYKTTPPVLDSDGSFLYSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Natch 68.0%; Score 1262; DB 21; Length 744; 
Best Local Similarity 75.3%; Pred, No. 2.3e-84; 
Natches 253; Conservative 15; Mismatches 40; Indels 28;
                                                                                                                                                                                                                                                                 Hoekstra DM, Loughney K, Stauton DE, Vazeux R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5: Page 174-176; 187pp; English.
                                                                                                   99WO-US28878.
                                                                                                                                                        980S-0203462
                                                                                                                                                                                                                                                                                                                WPI: 2000-422952/36.
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                                                                                                                                                                                                            (ICOS-) ICOS CORP.
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WO200032633-A1.
                                                                                                   02-DEC-1999;
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glome-tulonephritis; proliferative disorder; diabete nephropathy; 
oblaserulonephritis; proliferative vitreorethinopathy; myelofibrosis; 
collaserulonephritis; profiferative vitreorethinopathy; myelofibrosis;
                                                                                                                         human or citabilatory makeria (pr. 12 was produced by ERE Centrally) to human 1911-Fe. It was produced by ERE magnification (p. 121-Fe. It was produced by ERE magnification (p. 121-Fe.) and M. Anhaid prowittenspire, resulting the magnification (p. 121-Fe.) and M. Anhaid prowittenspire (p. 121-Fe.) and magnification in payments. The invention relieves non-locations and sideolders intrastructure of extraorrangement of the programment of the properties of the manual programment with $0.1 and $0.2 approximate or produce such antique research or the intranspire (p. 121-Fe.) and the produced or produce such actions to the intranspire (p. 121-Fe.) and the produced or produce such actions to the intranspire (p. 121-Fe.) and the produced or produce such actions to the intranspire (p. 121-Fe.) and intrinsical states (p. 121-Fe.).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 IMOKSQDNVTELYDVSISLSVSFPD-----VTSNMTIFCILETDKTRLLSSPFSIELED 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 -----SPNITDTMKFFLYVDKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 POPPDBRSPGLOEPKS----CDKTHTCPPCPABELGGPSVFLPPPKPKDTLMISKIPE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 VTCVVVDVSHEDPEVKPNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKMQVSLTCLVKGFYPSDIA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Gaps
                                                                                      This 54 kDa soluble fusion protein, termed hB7.2Fc, is composed of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.6%; Score 1255; DB 20; Length 477; 78.3%; Pred. No. 4.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
Example 3.1.1.3: Fig 3: 182pp: English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 KSLSLSPGK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 DPKSSDKTFTCPPCPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWYZIONE HINDER TERMINATION OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HINTHINITIES THE STREET THE STREET THE STREET STREE
                                                                                                                                                                                                                        77 FKNRVYLDTVSGSLJIY----NLTSSDEDEYEMESPNITDJMKFFLVV-------- 120
                                                                                                                                                                                                                                                                                                               208 FKGKATLTADKSSSTAYMQLSSLTSEDSADYYCARSNYYGSSYWFFDVWGAGTTVTVSSL 267
                                                                                                                                                                                                                                                                                                                                                                                             121 -----DKTHTCDPCPAPELLGGPSVPLFPPKPKDTAMISRTPEVTCVVVDVSHEDPEVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISKAKGOPREPOVYTLPPSRDELJKNOVSLJCLVKGFYPSDIAVEWESNGOPENNYKTTP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New molecules which bind B7.1 and B7.2 - useful to prevent and treat
Immune diseases including allograft rejection
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "human B7.2 (mature protein) extracellular
                                                                                                                                  25: Indels 21:
                                           DB 21; Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimnume disease; allergy; therapy; human, antibody; hB7.1fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "potential eukaryotic secretory signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "introduced by PCR cloning strategy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "human IgG1-Fc (hinge-CH2-CH3)"
                                           Score 1255.5; DB
Pred. No. 5.6e-84
                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sablon E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW90207 standard; Protein; 477 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187.2Fc soluble fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bosman A, Buyse M, Lorre K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-EP03791.
                                           67.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                  Matches 241: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 . . 245
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Chimeric - synthetic.
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                                                                                      Similarity
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                                           Query Match
Rest Local 8
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion protein of a splice variant of transforming growth factor-beta receptor, for inhibiting the growth factor, e.g. i
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanicola-Nadel
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90.7%; Pred. No. 6.1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cate R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEALHNHYTQKSLSLSPGK 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GOTWals P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AA245253, AA245254
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Matches 235; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Koteliansky V,
                                                             Homo sapiens
                                                                                                                           14-848-81
                                                                                                                                                                                                                                                      :6-1-NDF-91
                                                                                                                                                                                                                                                                                                              16-JUN-1998;
                                                                                                                                                                                         23-DEC-1999
                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                         This sequence is a fusion potential of the main transforation of the function 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 SSDE------DEYEMESPNITDTMKFFLYVDKTHTCPPCPAPELLGGPSVFLFPPKPK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 SSDECNDNIIFSEEYNTSNPDL------VDKTHTCPPCPAPELLGGPSVFLFPPKPK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19; Length 388;
                                                                                                                                                                                                                 fransforming growth factor-beta receptor fusion protein - used
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                                                             Sanicola-Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1251.5; DB
Pred. No. 6.1e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4: Mismatches
                                                             Koteliansky V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY54064 standard; Protein; 388 AA.
                                                                                                                                                                                                                                                      reat fibroproliferative disorders
                                                                                                                                                                                                                                                                                                        Claim 4; Page 19-20; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 HEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 HEALHNHYTQKSLSLSPGK 388
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                                                             Gotwals P,
                                                                                                                     WPI; 1998-609994/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
(BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 AA:
                                                                                                                                                          N-PSDB: AAV08999
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                                                             Cate R,
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The preset restance represents a spitch evitant of a retalt transforming growth factor beta (FGF-beta) type II receptor itsel to the Re portion of heam right. The fission uponed in an integer affaither for FGF-beta benefits of heam right of the FGF-beta benefits of heam right of the FGF-beta benefits of TGF-beta benefits of TGF-benefits of TGF-beta benefits of TGF-benefits of T
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of TGF-beta type II receptor variant/IgGl fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of TGF-beta, especially fibroprollierative diseases, e.g. renal, threacular or pulmonary fibrosis diabeth emphropathy; myelofibrosis; glomeralonephitis; prollierative vitreorethopathy; myelofibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Splice variant; rabbit; transforming growth factor-beta; TGF-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen vascular disease, e.g. systemic sclerosis, polymyositis, scleroderma, dermatomyositis or systemic lupus erythematosus; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.4%; Score 1250.5; DB 21; Length 388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 62-63; 69pp; English.
                                                                                                                                                                                                                                                      AAYS4063 standard; Protein; 388 AA.
                                    329 HEALHNHYTQKSLSLSPGK 347
                                                                   370 BEALBNEYTOKSISISPGK 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koteliansky V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09965948-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6-30N-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                   AAY54063:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                       AAY54063
                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                  Miss sequence is a festion protection of the relate transferrange growth forcer-feet seepror II (100°-feetRII) and an antibody Fe festion. The concept present is an example of a protection of the invention, which has been seen to the invention of the invention. Which has been seen to the invention of the invent
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                                                                                                                                                                                                                                                                              Transforming growth factor-beta receptor; Tey-beta receptor; arthritis; 
close procedin, throprolliferative disorder; diabetic nephropathy; 
glomerulonephritis; prolliferative vitreoretinopethy; myelofibrosis; 
objasqu vasoular disorder; therapy; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 DILMISRIPEVICOVODOSHEDPEVERNAVDGGEVENARTKPREEQVASTYRVGVELTV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 VKGEYPSDIAVBWESNOOPENWYKTTPPVLISEGSFELVSKLYDKSRMOOGNVFSCSVM 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSDE-----DEYEMESPNITDIMKFFLYVDKTHTCPPCPAPELLGGPSVFLPPPKPK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 STDECNDHIIPSEEVITSSPDL------VDKTHTCPPCPAPELLGGPSVFLFPPKFK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 DILMISRIPEVICOVODOSHEDPEVKENNYVDGVEVHNAKTKPREEDYNSTYRVVSVLTV 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 UKGFYPSDIAVEMESNGOPENNYKTTPPVIJSBGSFFLYSKLTVDKSRWOOGNVFSCSVM 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fransforming growth factor-beta receptor fusion protein - used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kotellansky V. Sanicola-Nadel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3e-84;
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90.7%; Pred. No. 7.3e-
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                                    AAW73513 standard; Protein; 388 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treat fibroproliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 18-19; 70pp; English.
                                                                                                                                                                                                                       Rabbit TGFbetaRII:Fc protein.
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                                                                                                                                                               (first entry)
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receptor (TOPT) partners comparison at Inthopiata prost factor (TOPT) exceptor (TOPT) at Action by the International Internation
      extracellular domain fused to a heterologous oligomerization domain for treating FGF., angiogenesis., or FGF receptor-mediated disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 EALEERPAVMTSP-----LYLEGGSGPGLQEPKSCDKTHTCPPCPAPELLGGPSVF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 LEPPKPKDTLAISRTPEVTCVVVDVSHEDDEVKFNMYVDGVEVHNAKTKPREEDVNSTYR 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKŢISKAKGQPREPQVYŢLPPSRDELTKN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 QVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFLYSKLTVDKSRAQQGN 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 TSSDEDEYEMESPNITDIMKFFLYV------DKTHTCPPCPAPELLGGPSVF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 PSNVPLKEVL-----WKKOKDKVAELENSEPRAFSSPK----NRVYLDTVSGSLTIYNL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 LEPPKPKDTIAISBTDEVTCVVVDVSHEDPEVKENMYVDGVEVHNAKTKPREBOYNSTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%; Score 1249.5; DB:
75.8%; Pred. No. 1.2e-83;
iive 12; Mismatches 32.
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Job time : 38.7806 secs
                                                                                                Claim 14; Page 58-59; 70pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     472 VFSCSVMHEALHNHYTQKSLSLSPGK 497
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Introduced the control of the control of
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                                                                                                                                                                                                                                                 110 DILMISETPEVECEVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEGYNSTYRVSVLTV 249
                                                                                          97 SSDE------DEYEMESPNITDTMKFFLYVDKTHTCPPCPAPELLGGPSVFLFPPKPK 148
                                                                                                                        149 DILMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREBOYNSIYRVVSVLTV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 VKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= FGF-R1_extracellular_domain
/Aocte= "The Ig I segment and acid box are deleted"
59..111
                                                                                                                                                                                                                                                                                                                                     LHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL7CL
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                                    Indels
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90.7%; Pred. No. 7.3e-84;
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22..257
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/label- 19_III_segment
258..265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 HEALHNHYTOKSLSISPGK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 HEALHNHYTQKSLSLSPGK 347
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Best Local Similarity
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06/1-60-8B	omcose wraten 5.1.3 Copyright (c) 1993 - 2003 Compagen Ltd.	OM protein - protein search, using sw model	Run on: January 28, 2003, 08:40:59 ; Search time 113.923 Seconds (VINDout alignment) (Alichout alignment) (6.162 Million cell updates/sec	Title: US-09-730-465-8 Perfect core: 1870 Sequence: I WANGSDAGRALGVIZVYCLLMHEALHMNTQKSLSLSEFOK 347	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 122226 seqs, 20178551 residues	Total number of hits satisfying chosen parameters: 122226	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match OM MAXIMUM AscchildM AscchildM Ascchild AscchildM Ascchild AscchildM Ascchi	The change .		Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Result Query No. Score Match Length DB ID Description	00.0 347 9 US-10-091-236-17	1251.5 67.4 388 10 US-09-734-300-9 1250.5 67.4 388 10 US-09-734-300-9	1249 67.3 859 1249 67.3 1158 1249 67.3 1168	1247 67.2 451 10 US-09-875-338-17 1247 67.2 698 10 US-09-875-338-9	1242 66.9 388 10 US-09-784-623-16 1242 66.9 492 10 US-09-85-899A-3	66.8 48.2 10 US-09-814-259-2 Sequence 2, 66.8 48.2 10 US-09-814-256-2 Sequence 2, 66.7 69.9 (US-09-935-868-22 Sequence 20, 66.7 69.4 (US-09-935-868-22 Sequence 20,	1238, 5 66.7 780 9 US-09-935-668-34 1238, 5 66.7 780 9 US-09-935-868-38 1238, 5 66.7 780 9 US-09-935-868-42

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FITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
Presenting Cell Driven Skin Conditions Using
Inhibitors of the COZ/LRA-3 interaction
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WIDDLIN TYPE: Floppy disk

WIDDLIN TYPE: Floppy disk

COMPATING REMONAL R
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Best Local Similarity 100.0%; Pred. No. 1.7e-123;
                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-111CP
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SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
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                                                                                                                                           NUMBER OF SEQUENCES: 8
                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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2IP: 02109-1875
                                                                                                                                                                                                                                                                                                                          CITY: Boston
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PRIOR APPLICATION WINHBER: 05 60/99.456
PRIOR FLITCHION WINHBER: 05 60/99.456
WINHBER OF SEQ. ID NOS: 8
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APPLICANT: Wallner, Barbara P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09796033
Patent No. US20020009446Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-730-465-8; Sequence 8, Application US/09730465; PatentyNo. US20020009449A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: SIGNAL
) LOCATION: (1)...(28)
US-09-796-033-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-796-033-8
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US-09-734-300-9

Cooper, Kevin D.

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APPLICANT: Responsor on Purrascenticals, Inc.
TLE OF INVENTIVE DEPRETATION SEED TO SEE A MAISSONISTS, and Methods of Making and Using
PILE REFERENCE: RES 2010
PLANE MARKET APPLICATION WOMBER: 105,979/35,868
CORREST FILING DATE: 2009-14:11
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TITIE OF TWENTON: Receptor Based Antaquists, and Methods of Making and Using
FILE REPERMENT SEES 2020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 NITDIMKFFLY------VDKTHTCPPCPAPELLGGPSVFLFPPKPKDILMISRTPE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         605 EFIFTTPRFAQGEIESGEPRSCDKTHTCPPCPAPELLGGPSVFLFPPRKDTLMISHTPE 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 VEWESING PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ 338
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                                                                        269 VKGPYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 328
                                                                                                                                                         310 VKGPYPSDIAVEMESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRNOGGNVFSCSVM 369
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190 DILMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREBOYNSTIRVVSVLIV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 26; Gaps
                                             209 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.3%; Score 1249; DB 9; Length 859; Best Local Smallarity 78.3%; Pred. Ro. 2e-80. 2e-80; Matches 242; Conservative 11; Manatches 30; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
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; Sequence 26, Application US/09935868
; Patent No. US20020164690A1
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09935868
Patent No. US20020164690A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
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US-09-935-868-7
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310 VKGFYPSDIAVEMESNGQPENNYKTTFPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVW 869
310 VKGFYPSDIAVEMESNGQPENNYKTTFPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVW 869
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TITLE OF INVENTION: Variant Type II TGF-Beta Receptor Fusion Proteins
                                                                                          Variant Type II TGF-Beta Receptor Fusion Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1251.5; DB 1
Pred. No. 5.4e-81;
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CURRENT FILING DATE: 2000-12-11
                                                                                                                 FILE REFERENCE: A058CT
CURRENT APPLICATION NUMBER: US/09/734,300
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: 60/089,452
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PRIOR FILING DATE: 1998-06-16
NUMBER OF SEQ ID NOS: 13
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Patent No. US20020004037A1
    Sequence 9, Application US/09734300
Patent No. US20020004037A1
GENERAL INFORMATION:
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Best Local Similarity 90.7%;
Matches 235; Conservative
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NUMBER OF SEQ ID NOS: 13
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                                                                            BIOGEN, INC.
                                                                                                                                                                                                                                                                                                                                                   CRGANISM: Homo sapiens
US-09-734-300-9
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                                                                                               TITLE OF INVENTION:
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US-09-734-300-8
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LENGTH: 388
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                                                                                                                                                                                                                                                                                                      LEMCTH 388
                                                                            APPLICANT:
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1044 VSNRALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 1103
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                                                                                                            23 VSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWE 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 SPNITDTMKFFLYVDKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22] PKS------CDKTHTCPPCPAPELLGGPSVFLFPPRRYFCTMISRTPEVTCVVDV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: fusion construct
15. OTHER INFORMATION: fusion construct
16.05-05-815-338-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17. Application by/0873338
Parent No. US20000950434
GERBEAL PROMETRIES ILL R.
APELCONT CHARGE, IMAR
APELCONT FIRESE, 2098UA N.
APELCONT TRACE, 2098UA N.
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APELCONT TRACE, 2008UA N.
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TITLE OF WRESPONDED PREMIORATED INC.
TITLE OF WRESPONDED TO 2000 TO CARROLL AND METHODS OF Meking and Using
CHERRY PRINCIPLO WRESE. 18679/35,869
PRICE PRICE TITLE OF THE TOTAL TO THE TOTAL 
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                                                                                                                                                                                                                                                                                                                                                                            Query Watch 67.3%; Score 1249; DB 9; Length 1158; Best Local Similarity 79.3%; Prefed, No. 2.78-80; Matches 34; Conservative 11; Mismatches 30; Indels 22;
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CURRENT FILMS DATE: 3002-40-11
PRICOR APPLICATION NUMBER: PCT/US99/22045
PRICOR FILMS DATE: 1999-09-22
NUMBER OF SED ID NOS: 52
SOUTHAME: PATENTIN VORTSION 3.0
SSOUTHAME: PATENTIN VORTSION 3.0
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Patent No. US20020164690A1
GENERAL INFORMATION:
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SEQ ID NO 24
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Best Local Similarity 79.3%
Matches 242; Conservative
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US-09-935-868-26
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287 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 346

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163 VYDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 222

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186 PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREDQYNSTYRVVS 245
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APPLICANT: COLLIES, David S.
TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
TITLE OF INVENTION: DISPASES
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APPLICARY: THE SALLY DOBERN PAYED A
APPLICARY: TRUNKSI, ALESSEDED
APPLICARY: TRUNKSI, ALESSEDED
TITLE OF INVENTION: HEARBEIGE FUSION PROTEINS AND USES
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CORRENT PARLICATION WORREN: US/09/784, 623

PRIOR MPELICATION WORREN: 05/09/134

PRIOR FILING WORR: 1959—07/05 97/03131

PRIOR FILING DATE: 1959–07/05 97/03131

PRIOR PILING DATE: 1959–07/10 97/03131

PRIOR FILING DATE: 1959–07/10 97/03131

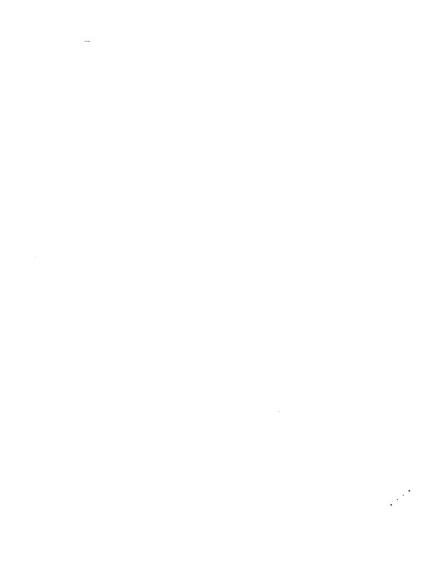
PRIOR FILING DATE: 1959–07/10 97/03131

PRIOR FILING DATE: 1959–07/10 97/03131
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CURRENT APPLICATION NUMBER: US/09/845,899A
CURRENT FILING DATE: 2001-04-30
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SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 1999-01-13
PRIOR APPLICATION NUMBER: US 60/043,948
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PRIOR APPLICATION NUMBER: US 60/038,915
PRIOR FILING DATE: 1997-02-21
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Patent No. US20020147326A1
GENERAL INFORMATION:
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US-09-784-623-16
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Patent No. US2002009454A1
GENERAL INFORMATION:
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APPLICANT: Hershenson, Susan
APPLICANT: Bevilacqua, Michael P.
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301 DGSFFLYSKLIVDKSRRQQGNVFSCSVMHEALARHYTQKSLSLSPGK 	HYTOKSLSLSPGK HYTOKSLSLSPGK	HYTOKSLSLSPGK	q	585	GOPREPQVYTLPPSRDELTRNQVSLTCLVRGFYPSDIAVEWESNGQPENNYRTTPPVLDS
645 DGSPPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	HYTOKSLSLSPGK	HYTOKSLSLSPGK	οy	301	DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
	Casech countlated: Tanner 20 2002 08:52:01	Search completed: January 28, 2003, 08:53:01 Job timm : 114.923 secs	qq	645	DGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTOKSLSLSPOK



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Sequence 15, April 18, April 18, April 19, Apr
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OPERATING SYSTEM: PC-DOX/NS-DOS
SOFTWARE: Patentin Release 11.0, Version 11.25
COMPARET APPLICATION DAYN.
THINE DAYN.
CLASSIFICATION: 514-199.
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PRICE APPLICATION PARS.
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-940-861-43
Sequence 43, Application US/07940861
Patent No. 5547853
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REGISTRATION NUMBER: 27.794
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TELER: 14-8367
INPORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
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COUNTER: New YORK
COUNTER: 10022-626
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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875 Third Avenue
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Sequence 4.7 April
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Sequence 5.5 
                                                                                                                                                                                                                                                                                                January 28, 2003, 08:38:45 ; Search time 15:6935 Seconds (without alignments) 650.773 Million cell updates/Sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1856-09-730-465-8
1856-09-730-465-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Issued_Patents_A_A_A_SA_COMB_pep.*
| Cogn_2_6/pcdata_A_//iaa/SA_COMB_pep.*
| Cogn_2_6/pcdata_A//iaa_SB_COMB_pep.*
                                             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105.00 (10.1.9) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1.1) (10.1
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US-08-459-512-43
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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us-09-730-465-8.rai

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61 DKVARLENSERRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKPFLYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DKVARLENSERAPSSFKNRVILDIVSGSFIINITASSDEDEVENSBENITDINKFFLVV 120
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                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                               1 MVAGSDAGRALGVLSVVCLLHCFGFISCFSOOIYGVVYGNVTFHVPSNVPLKEVLMKKOK 60
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                                                                                                                                                                                                                                                     100.0%; Score 1856; DB 1; Length 347;
100.0%; Pred. No. 3.2e-163;
1ve 0: Mismatches 0: Indels 0
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APPLICANT: WILLES, CEENT P.
APPLICANT: MILLES, CEENT T.
TITLE OF THEWETHOLE, CEENT T.
MILLES OF THEWETHOLE TO CONTINUE OWALIN OF LAMBHOCITE
TITLE OF THEWETHOLE TO WORTHOM ASSOCIATED AFFICEN 3
MURRER OF SEQUENCES.
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PRIOR APPLICATION NUMBER: PCT/US92/U2050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JABER: US 07/567,971
12-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/459,657
FILING DATE: 02-JUN-1995
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Patent No. 5914111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 1448367
INPORATION FOR SEG ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
                                                                                                               LENGTH: 347 amino acids
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                                                                                                                                                                                  MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy of
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Best Local Similarity
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FRY: U.S.A.
10022-6250
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                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                            1 MVAGSDAGRALGVISVVCLLHCFGPISCPSQQIYGVV7GNV7PHVPSNVPLKEVLWKKQK 60
                                                                                                                                                                                  1 MVAGSDAGRALGVISVYCLIHCFGFISCFSQQIYGVYGNYTFHVPSNVPLKEVLMKKQK 60
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                                                                                                                    Gaps
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                                                                   Ouery Match 100.0%; Score 1855; DB 1; Length 347; Best Local Similarity 100.0%; Pred. No. 3.28-153; Matches 47; Conservative 0; Mismatches 0; Indels 0;
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APPLICAMY SERVICES CHARGE DESCRIPTION OF LYMPHOCTE
APPLICAMY ROSA, MAGREE D.
APPLICAMY ROSA, MAGREE D.
TITLE OF INVENTION: COULD SERVINE DAMIN OF LYMPHOCTE
TITLE OF TWENTION: FUNCTION ASSOCIATED A
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FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
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APPLICATION DATA:
PRIOR APPLICATION DATA:
PILIUM:
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
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FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
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; Sequence 43, Application US/08459512
; Patent No. 5728677
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Pish & Neave
STREET: 875 Third Avenue
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    MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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10022-6250
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CLASSIFICATION:
                      US-07-940-861-43
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61 DKVAELENSEPRAFSSFKNRYLDTVSGSLTIYNLTSSDEDEYEMSPUITDTWKFFLYV 120
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Pred. No. 3.2e-163;
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                                                                                                                                     MBER: PCT/US92/02050
12-MAR-1992
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STREET: 60 State Street, Suite 510
APPLICATION NUMBER: US/08/460.132
FILING DATE: 02-7UN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                MBER: US 07/770,967
07-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: B151CIP2
                                                                                               US 07/940,861
                                                                                                                                                                                                             UMBER: US 07/667.971
12-MAR-1991
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: Sequence 8, Application US/08466465
; Patent No. 6162432
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TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
                                                                                                                                                                                                                                                                                                                                                        NAME: HALEY, James F., Jr. REGISTRATION NUMBER: 27,794
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INFORMATION FOR SEQ ID NO: 43:
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Best Local Similarity 100.0%;
                                                                                                             21-0cT-1992
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LENGTH: 347 amino acids
TYPE: amino acid
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US-08-460-132-43
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APPLICATION NUMBER: (
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                                                                                               APPLICATION NUMBER:
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FILING DATE: 07-OCT
                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1856; DB 2; Length 347;
100.0%; Pred. No. 3.2e-163;
Live 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
                                                                                          NAME: HALEY, James F., Jr.
REGISFERATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B15ICIP2
TELECOMMUNICATION INFORMATION:
                       US 07/770,967
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               Sequence 43, Application US/08460132
Patent No. 5928643
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BIOGEN, INC.
APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSA, Margaret D.
                                      FILING DATE: 07-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.

Best Local Similarity 100.

Matches 347; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein
US-08-459-657-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
PREOR APPLICATION DATA:
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
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US-08-460-132-43
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TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
NUMBER OF SEQUENCES: 43
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PCT-US92-02050-43
                                                               CORRESPONDENCE ADDRESS:
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US-09-131-247-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNNYVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.1 GOPREPOVYTEPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVAGSDAGRALGVLSVVCLLHCFGFISCFSQQIYGVVFGNVTFHVPSNVPLKEVLWKKQK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
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                                                                               COMPUTER READABLE FORM
MADINE THER FLORPWISH
COMPUTER: IMP RC COMPUTED: COMPUTED: IMP RC COMPUTED: OSFWATHOR STEER: FC-DOX/MS-DOS
SOFWATHOR STEER: PC-DOX/MS-DOS
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FILING DATE: 06-0CT-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,969
FILING DATE: 07-0CT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/862,022
FILING DATE: 12-APR-1992
                                                                                                                                                                                                       APPLICATION NUMBER: US/08/466,465
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GENERAL INFORMATION:
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APPLICANT: WALLNER, Barbara P.
MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
                                                                                                                                                                                   URRENT APPLICATION DATA:
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Matches 347; Conservative
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US-08-466-465-8
                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                       Massachusetts
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Best Local Similarity
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                                                               02109-1875
                                               OSA
       Boston
                                                                                                                                                                                                                               FILING DATE:
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                                               COUNTRY:
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61 DKVAELENSEPRAPSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLYV 120 61 DKVARLENSERRAFSSFKNRVYLDTVSGSLTIXNLTSSDEDEYEMGSPNITDTMKFFLVV 120 12. DKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 180 121 DKTHTCPPCPAPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 180 181 GVEVHNAKTKPREEDYNSTYRVVSVLTVLHODWINGKEYKCKVSNKALPAPIEKTISKAK 240 241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 300 1 GOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTPPVLDS 300 Gaps 1 MVAGSDAGRALGULSVVCILHCFGFISCFSOOIYGVVYGNVTFHVPSNVPLKEVLWKKQK 60 1 MVAGSDAGRALGULSVVCLLHCFGFISCFSQQIYGVVYGNVTFHVPSNVPLKEVLWKKOK 60 ö Length 347; Indels 301 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347 Score 1856; DB 5; Pred. No. 3.2e-163; ; Mismatches 0; SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US92/02050 FILING DATE: 19920312 Query Match
100.0%; Score 1856;
Best Local Similarity 100.0%; Pred. No. 3.2
Matches 347; Conservative 0; Mismatches STATE: New York
COMPITE: New York
COMPITE: REGARDER TOBE
MEDIAN TITE: ELORGE TOBE
COMPITE: THE E CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NOBER: US 07/667,971
PILING DATE: 12-MAR-191
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/770,967 FILING DATE: 07-OCT-1991 ATYORNEY_AGENT INFORMATION: NAME: HALEY, James F., Jr. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: B151CIP2 TELECOMMUNICATION INFORMATION: TELEPHONE: (212)715-0600 TELEFAX: (212)715-0673 TELEX: 14.8367
TELEX: 14.8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: AMINO ACID ADDRESSEE: Fish & Neave STREET: 875 Third Avenue

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Sequence 16, Application US/09131247

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315 DCVEVHNAKTYRPREQYNSTYRVVSVLTVLHODMLMGKEYRCKVSNKALPAPIEKTISKA 374
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TITLE OF INVENTION: P-SELECTH LIGANOS AND RELATED MOLECULES
THERE OF INVENTION: AND METHODS
CORRESSED FOR THE ALCHARGOS P.C.
STREETS AND THE ALCHARGOS P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ouery Match 65.8%; Score 1239.5; DB 4; Length 4 Best Local Similarity 100.08; Pred. No. 3.8e-106; Metches 228; Conservative 0; Mismatches 0; Indels Metches 288; Conservative 0; Mismatches 0; Indels
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                                       - MEDIUM TERE: Flopowy disk
COMPUTE: INM CC COMPALIDE ON
PURBATHAR: PATENTIA RELEASE 11.0, VETSION 13.30
SOFTWARE: PATENTIA RELEASE 11.0, VETSION 13.30
APPLICATION NUMBER: US/09/193139
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COMPUTER: IBM PC compatible
OPERATIEN: SYSTEM: PC-DOS/MS-DO
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A006 PCT CIP
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: A006 PCF CIP
PRILING DATE: 09-MXY-1997
PILLING DATE: 09-MXY-1997
APPLICATION NUMBER: 60/1017,466
FILLING DATE: 10-MXY-1996
APPLICATION PROPRATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 679-2000
TELEFAX: 617 679-2838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 482 amino acids
TYPE: amino acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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CITY: Boston
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ANTI-SENSE:
JS-09-189-129-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US96-10043-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 VLTVIHQDMINGKEYKCKVSNKALPADIEKTISKAKGOPREPQYTLPPSRDELTKNOVS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 LTIYNLYSSDEDEYEMESPNITDTW-----KFFLYV----- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 MCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 MEADQPVSLTNMPDEGVMVTKFYFOEDEAAAEPKSSDKTHTCPPCPAPELLGGPSVFLPP 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 LTCLVKGFYPSDIAVEWESNSQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGNVFS 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 NQLVAGYLQG------PAVNLEE-----KIDVVPIE------PHALFLGIHGGK 65
                             66.9%; Score 1242; DB 4; Length 388; 65.0%; Pred. No. 1.6e-106;
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Patents No. 53,33027
PAPICART: PAPICATION CONTROL OF SEASON CONTROL
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BARLIER A PETCHTON NAMES: 1937-08-06

BARLIER A PETCHTON NAMES: PCT-708-97

ROMERS: PCT-708-97

ROMERS: PCT-708-97

ROMERS: PCT-708-97

SERVINES: PCT-708-70

SERVINE
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Matches 249; Conservative 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: Massachusetts
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CORRESPONDENCE ADDRESS:
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US-09-131-247-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 388
TYPE: PRT
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105 MESPNITDTMKFPLYV------DKTHTCPPCPAPELLGGPSVFLFPPKPDT 150
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                                                                                                                                                                                                                                               211 ODMINGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVK 270
                                                                                                                                                                                                                                                                                                                                    448 LNAPNVIDTGHNPAVINISSEPYPGEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 507
                                                                                                                                                      151 IMISRTPEVICOVODVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 210
                                                                                                                                                                                                                                                                     72 RAFSSFKNRVYLDTVSGSLTLYNLTSSDEDEYEMESPNITDTMKFFL------YVD 121
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Best Local Similarity 89.5%; Pred. No. 7.3e-106;
Matches 230; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "L'ESSY-DIA CALLO PC/TUSS930866
SEGRENT INFORMATION: TO CALL STATE SECRET US)
APPLICANT PCTOMONE, TO. (All STATE SECRET US)
APPLICANT: MOCHA, MACHAEL B (US ONLY)
TITLE OF TUNENTYON: STABLILIZED DIMBO OF KIT LIGAMO AND
NUMBER OF SEQUENCES: 16 "IT-17EK-2 LIGAMO
NUMBER OF SEQUENCES: 16
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COMPUTES: IIBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Wersion #1.30
SOFTWARE: Patentin Release #1.0. Wersion #1.30
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTOWNER/AGENT INFORMATION:
NAME: Haley Jr. James F
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEC ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                            331 ALHNHYTOKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                  688 ALHNHYTOKSLSLSPGK 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 424 amino acids
amino acid
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 PLYVDKTHTCPPCPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 ---CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WYUDGVEVHNAKTKPREBQYNSTYRVVSVLTVLHODWLNGKBYKCKVSNKALPAPIEKTI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12: Indels 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1239; DB 5; Length 442;
Pred. No. 3.7e-106;
8; Mismatches 12; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.8%; Score 1239; DB 4; Length 704;
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/590,656
                      APPLICATION NUMBER: PCT/US96/10043
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JMBER: 60/137,889
1999-06-07
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APPLICANT: Cerrett, Douglas P.
APPLICANT: Borges, Luis G.
APPLICANT: FONSIOW, III, WILLIAM C.
TITLE OF INVENTION: TER ANTAGONISTS
FILE REPREBAUE: 2900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09590656
Patent No. 6413932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.8%;
Best Local Similarity 82.1%;
                                                                                                                                                                             NAME: Lech, Karen F.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
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CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
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PRIOR FILING DATE: 1999-0
NUMBER OF SEQ ID NOS: 2
SOPTWARE: PATENTIN VEY: 7
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US-09-590-656-2
                                                                       CLASSIFICATION:
                                                                                                                                FILING DATE: 1.
CLASSIFICATION:
                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-DS96-10043-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 704
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Query Match TYPE: PRT

Db 199 KTHTCPPCPAPELLGSPSVPL.PPKPKDFLALSRPBVTCVVDVSHEDPBVKPWVDC 258	Oy 182 UEVHNAKTKPREDOYNSTYRVVSVLTVLAGDMLACKEYKCKVSNKALPAPIEKTISKAKG 24.1 10	Oy 24.2 OPREDOVPTLPPSEDELTRNOVSLTACLYKGPPSEDLAVERESNODFENHYRTFPPULDSD 301 Db 319 OPREGVYTLPSSIDELTRNOVSLTACKYREPPSDLAVERSSNODFENHYRTFPULDSD 379	Dy 302 OSFPLYSKLIVDRSSRROOGNVPSOSVMBDLINNHYVORSILSEDGK 347 Bb 379 GSFPLYSKLIVDRSSRROOGNVPSOSVMBDLINNHYVORSILSEDGK 424	RESULT 13 FGT-1866-10043-11 ; Sequence 11. Application FC/TUS9610043	GENERAL TROPRINTOR: TITLE OF INVENTION: SELECTIVE LICANOS AND RELAYED MOLECULES TITLE OF INVENTION: AND METHODS TITLE OF SEQUENCES TITLE OF SEQUENCES TITLE OF SEQUENCES TOWNERS OF SEQUENCES OWNERS OF SEQUENCES:	ADDRESSE: Fish & Richardson P.C. FISHER: 225 Franklin Street CITY: Boston FROM: MA	COUNTRY USA 2 TEP 02210-2804 COMPUTER ERRIGHE PORM:	MEDIUM TYPE: Ripper disk COMPUTER: LIM PC COMPATIBLE OPERATING SESTEM: PC-1005/MS-DOS	SOFWARE: Patentin Release #1.0, Version #1.30 CURREN APPLICATION DATA: RPHICATION NUMBER: PCT/US96/10043 FFITAM DATE:	CLASSIFICATION PROGRAPHICATION DATA: ; APUR APLICATION NUMBER: US 60/000,213	FILING DATE: 11-JUN-1995 CASSEDCATON: ATTORICY CASETY INFORMATION: NAME (A CASETY INFORMATION:	NAME: LEGHT MATERI F. REVERENCE/DOCKET MATERIAL TELECOMOUNICATION INFORMATION.	TRLEPHORE: 617/542-5070 TRLEPHORE: 617/542-5070 TRLERS: 017/54-5006 TRPORANTION POR SED ID NO: 11		TOWNERS THE STATE OF TELEVALL. ** WIRCHIE TYPE: Probein PCT-US96-10043-11	Ouery Match Bost Local Similarity 78-89, pred. Mo. 4.1-06; Matches 239, Conservative 10; Mismatches 19; Indels 35; Gaps	LENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEY	106 ESPNITDTWKFFLYUDKTHTCPPCDADELLGGPSVFLFPPRFKDTL	Db 204 EGEFKSCDKTHTCPPCPAPELLGGPSVPLPPFKFKDTLMISKTPEVTCVVVD 235
Db 146 RSIDAFKDPWARSETSDCWSSTLSPEKDSRVSVTKPBMLPPWADPEFKSCD 198	dy 122 KRHYCPPCPAPELLGGSYBLPPDKPKOTIAISRTBWTCWWOISHEDPEWENNWUG 181 DD 199 KHHTGPCPCRELLGGSYBLPPPRKRTIAISRTBWTCWWOISHEDPEWENNWUG 258	OY 182 VEWHANTREPRESONSTITIVENDEN AGRETICATION OF 182 VEWHANTREPRESON 141	OY 242 OPREPOVITLEPSREELIRANOVSLECLYKGPYPSDIAVBMESNOOPBINNYKTTPPVLDSD 301 319 OPREPOVITJPSREELIRANOVSLCUKKEPPSDIAVBMESNOOPBINNYKTPPVLDSD 378 bb 319 OPREPOVITJPSREELIRANOSLCUKKEPPSDIAVBMESNOOPBINNYKTPPVLDSD 378	Oy 300 GSTILEALTHYRERONDONSCONNINEMENTROGEGEROR 347 DD 319 GSFILESKLIVERSRONDGGWYEGSFUNIEMENTROGEGEROR 224	REBULT 12, September 2, September 2, September 2, September 2, Application PC/FUSS503866 (September 2, POPRMSAL PROMATOR) FOR PARTICIANT: CYTORNAL IDC. (All States except US)	: APPLICANT: NOCAE, KTAIL (US ONL) APPLICANT: LODELI, RODELT B (US ONLY) TITLE OF INVENTION: SYBALIZED DIMEN OF ET LIGAND AND TITLE OF INVENTION: FIT-3/FEL-2 LIGAND	NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSER: FF & New Ye	STREET: 1251 Avenue of the Americas CITY: New York STATE: New York	CONTRY: United States of America 2010FFK: 10030 COMPUTER REALABLE FORM: MEDITH TYPE: Florar disk	COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC JOS/AMP-DOS OPERATING SYSTEM: PC JOS/AMP-DS SOFTWARE: Factorin Release #1.0, Version #1.30	CURRENT APPLICATION DATA: ** APPLICATION INMER: PCT/UIS95/03866 FILIAM DATE:	PRIOR APPLICATION DATA: APPLICATION NUMBER: 08 08/220.379 FILING DREE: 28-NAR-1994	: ATTORNEY/ACENT INFORMATION: NAME: Heby Jr. James F STREATION NAMES 27.7.5 REFERENCY NAMES: CYLOMEG/2	TELECHOMICATION THORMATION: TELECHOMICATION TSORANICON: TELECHOMICATION TSORANICON: TELECHOMICATION TO MOD 14.	SQUIRNCE CHARGERISTICS: LIBERTIE: (14 main acid acids TYPE: Interest TYPE: Interest	: WOLBCULE TYPE: protein PCT-US95-03866-14	Ouery Watch Best Local Similarity 82.5%; Pred, No. 3.99-106; Best Local Similarity 82.5%; Pred, No. 3.99-106; Matches 236; Conservative 7; Mismatches 26; Indels 17; Gaps 2;	OY 72 RANSERKHWYLDTWYGGLITYNLISDEDERHERPNITDTMKFFL	0y 122 KTHYCPPCPAPELLGGPSVFLEPPKFKDTLMISRTPEWTCVVVDVSHEDPEVKFNMYUG 181

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119 XVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVXXDVSHEDPEVKFNHY 178
                                                                                                                                                                                                                                       179 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTLSK 238
                                                                                                                                                                                                                                                                                                                                                                                                          512 VDGVEVHNAKTKRREBOYNSTYRVUSVLTVLHODMENGKEYKCKVSNKALPAPIEKTISK 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 AKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 AKGQPREPQVYTLPPSKDELTKNOVSLTCLVKGFYPSDIAVEWESKGQPENNYKTTPPVL 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 RIPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDML 214
                                                                                                      Gaps
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                 Length 680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TOTANG, PREEZ COMING PROSPECT ASONIE THILD OF STREET COMING PREEZ COMING PROSPECT ASONIET COMPANY C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        632 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 680
                                                                                                      1; Indels
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COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                 Score 1238; DB 4;
Pred No 8 6e-106;
                                                                                              0; Mismatches
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NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31.171
REFERENCE/DOCKET NUMBER: SEC P50349-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
TELEPAX: 610-270-5090
99.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 488 amino acids
TYPE: amino acid
                                                                                              Matches 228; Conservative
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Best Local Similarity 92.5%
Matches 234; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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MOLECULE TYPE: protein
US-08-776-511-2
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                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-776-511-2
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                                                   NAME/KEY. LICAM(18/17)(9f d'asion protein

CHER INFORMATION: amino acid residues 1-453 —

OTHER INFORMATION: (1/OM(18/13)), amino acid residues 454-680 — amino

OTHER INFORMATION: acid residues 216-442 of human 1gGl heavy chain
        16 VSHEDPEVKFWHYUGVEVHNAKTKPREBOYNSTYRVVSVLTVLHODMLNGKEYKCKVSN 225
                                                                                                                                                                           226 KALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Teres Joffrey M.
APPLICANT: MCCELLAND Alan
TITLE OF INVESTION: Multimerte Rorms of Human
TITLE OF INVESTION: Milnovirus Receptor Protein
NUMBER OF SEQUENCES: 20
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COMPUTER: Dell Optifiex GX1
OPERATING SYSTEM: Windows 95
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FILING DATE: 05/24/91
FILING DATE: 07/26/238
FILING DATE: 07/20/90
ATORNEY/ACBATINCDEMATION:
RMG: DATABRA A. Shimel
REGISTRATION NUMBR: 29,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08227496C
Patent No. 6130202
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CLASERICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
PRILING DATE: 06/22/92
APPLICATION NUMBER: 07/003.069
APPLICATION NUMBER: 07/104,984
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TYPE: amino acids
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FRACMENT TYPE: complete sequence
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TELECOMMUNICATION INDOMATION:
TELEPHONE: (200) 812-549
INDOMATION FOR SEQ ID NO: 13:
SEQUENCE CHRACTERISTICS:
LEWGH SECTION SECTION OF THE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: diskett
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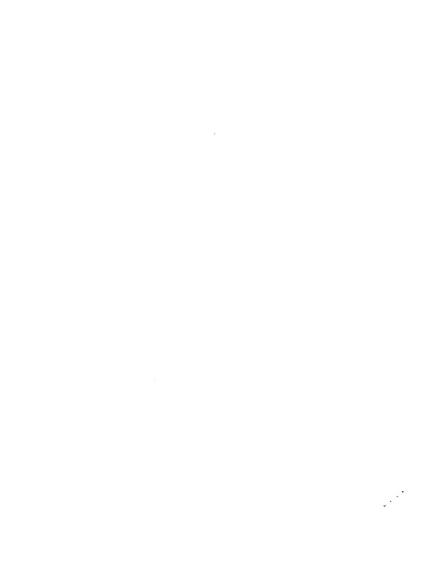
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us-09-730-465-8.rai

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g	8	296 RIPEVICVVODVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSTYRVVSVLIVLHQDWL 355	355
63	215	215 NGKEYKCKVSNKALPÅPIEKTISKAKGOPREPQVYTLPPSRDEL#KNQVSLTCLVKGFYP 274	274
qq	356	356 NGREYKCKVSNKALPAPIEKTISKAKGOPREPQVYTEPPSRDELTKNQVSL7CLVKGFYP 415	415
οy	275	275 SDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN 334	334
qq	416	416 SDIAVEWESNGOPENNYKTTPPVLDSDGSFELYSKLTVDKSRWQOGNVFSCSVMHEALHN 475	475

Search completed: January 28, 2003, 08:40:11 Job time: 17.6935 secs

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US-09-730-465-2_COPY_50_65		I PLKEVLWKKQKDKVAE 16	
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Total number of hits satisfying chosen parameters: 283224 segs, 96134422 residues Searched:

2770

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Cooper	Query	Query Mortob Tongth	8	4	ac) talend
. i	Score	March	Themat		97	peace thereu
1	28	33.3	12	2	869123	proton-translocati
6	27	32.1	-	?	154945	gene C protein - E
e	25	29.8	_	~	A39308	i.
7	24	28.6	-	6	P00445	
'n	24	28.6	15	2	S36888	
9	24	28.6	-	?	E49037	TcR delta chain V-
7	23	27.4	1	?	S21240	alpha-glucosidase
œ	23	27.4	15	~	S21202	glucan 1,4-alpha-g
6	23	27.4	-	~	B56891	gamma 2 gliadin -
10	22	26.2	-	2	803405	ger
11	21	25.0		CI	A60356	118K stomach cance
13	21	25.0	13	~	S60046	early nodulin 40 -
13	21	25.0	-1	-	OMWAPP	polistes mastopara
14	21	25.0	15	C4	833781	tat
15	21	25.0	16	C4	G45681	orf 61.1 - phage T
16	20	23.8	10	C4	E49033	T-cell receptor ga
17	20	23.8		c	PA0116	
18	20	23.8	11	2	PQ0731	unidentified 5.7/3
19	20	23.8	7	2	A26093	
20	20	23.8	-	C	JS0424	ep.
21	20	23.8	7	5	C60414	somatostatin - sli
22	20		-	2	B60842	somatostatin 1 - c
23	20	œ.		2	A60622	ds -
24	20	23.8	14	63	A60840	somatostatin I - E
25	20	œ.		2	800172	somatostatin I - s
56	20	23.8		2	B83836	hypothetical prote
27	20	23.8	16	?	A28144	ribosomal protein
38	50	23.8		2	H29501	fibrinopeptide A -
53	19	22.6	12	C	158273	thyroglobulin - ra

	histone Hla - mous	hemocyanin chain 2	hemoglobin beta ch	fructose-bisphosph	T cell receptor al	7 alpha-hydroxy-4-	homeotic protein G	mastoparan B - hor	T-cell receptor ga	probable trpEG lea	gene HEXA protein	enkephalin precurs	lactose phosphotra	probursin tetradec	1g H chain V-D-J r
B35245	A35245	A61308	PN0118	PA0102	PH1788	A45103	E37290	S14336	F49033	LFTWWE	164829	A32734	E39778	JH0328	PH1626
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30	31	32	33	34	32	36	37	38	39	9	4.1	27	ç,	7	5

ALIGNMENTS

RESULT S69123

proton-translocating transhydrogenase - Rhodospirillum rubrum (Iragment) C:Species: Rhodospirillum rubrum	vision 24-Apr-1998 #text_change 24-Apr-1998		R; Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.	200
proton-translocating transhydroge C; Species: Rhodospirillum rubrum	C;Date: 10-Mar-1998 #sequence_rev	C.Accession: S69123	R; Digale, C.; Hutton, M.; Jones,	Rur J Biochem 228 719-726, 10

EUI. U. BLOCHEII. 228, 713-729, 1333	A; Title: Properties of the soluble polypeptide of the proton-translocating transhydro	eference number: S69123; MUID:9525277; PMID:7737169	A;Accession: S69123	A; Status: preliminary	A; Molecule type: protein	esidues: 1-12 <dig></dig>
pre . o . pre	A; Title: Pr	A; Reference	A; Accession	A; Status: p	A; Molecule	A; Residues:

000	uery M est Lo. atches	atch cal Sim	118	rity nserva	Query March 33.3%; Score 29; DB 2; Length 12; Best Local Similarity 50.0%; Pred, No. 2.5e+02; Matches 4; Conservative 3; Mismatches 12; Indels Marches 12; Marches 12; Marches 13; Mismatches 14; Mismatches 15; Mismatc	Score : Pred. 1	28; No.	DB 2 2.5e+	 engt	h 12; dels	 Gaps	0
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ڡ	3	DVVWKV	- 8	10								

RESULT 2 IS4945

ome C protein. Expendicals coll (frogens).

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Query Match 32.1%; Score 27; DB 2; Length 14; Best Local Similarity 45.5%; Pred No. 4.189 40; Indels Morfoles 5. Conservative 4; Mismatches 62; Indels Morfoles 5.

ö Gaps

A39308 glycine reductase (EC 1.4.99.-) sulfhydryl protein C, alpha chain - Clostridium stick 2 LKEVLWKKOKD 12 1 LKEVIMEKKHE 11 RESULT 3

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"also "processions (pr. 20.1.20); I relatina 'thermocayloliquefacten' (fragent); Cibnel. 20.2.20; "Annual Procession of Cibnel. 20.2.20; "Annual Procession of Cibnel. 20.2.20; "Annual Procession; "Annu
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Maria Blocken 2019-256, 1962-556, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56, 1962-56
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MAlternate names esco-alpha-1-qluocaidase 1
Ciptei 2.3 Mov-1998 sequence_revision 01-Wov-1996 fract_change 21-Aug-1998
Chocesion: 2.31707
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A. Nesa idues : 115 - 1200 
A. Cross - Veferiones : GB: 2800553 : NID:9246296 : PIDN:AAR21551.1; PID:9246397 
A. Cross - Veferiones : GB: 2800553 : NID:92462997 
A. Cross - Veferiones : GB: 2800553 : NID:9246299 
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C:Superfamily: alpha-glucosidase: alpha-amylase core homology
C:Keywords: qlycosidase; hydrolase
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A.Molecule type: protein
A.Molecules 1.15 < SQUD.
A.Experimental source. AVCC 12016
C.Superfamily: alpha-glucosidase; alpha-amylase core homology
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27.3%; Pred, No. 1.4e+03;
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Pred. No. 2e+03;
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llarity 57.1%; Pred. No. 1.2e+03;
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A; Experimental source: brain
C; Superfamily: urotensin II
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entry modulin 40 - spring vetch

19. Alternate anses Spring vetch 2

19. Alternate anses Spring vetch tars, Spring a strong setting active (spring vetch, tars)

19. Alternate anses Spring vetch, tars, Control of the strong setting setting (spring vetch, tars)

19. Aprel 1997 setting vetch and target and target setting setting and target setting set
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Pred. No. 3.7e+03;
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Pred. No. 2.8e+05;
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A.Moleoule type: mRNA
A.Residues: 1-4 C4RP
A.Crossidues: 1-4 C4RP
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A; Residues: 1-14 <HIR>
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A)Accession: A60356
A;Molecule type: protein
A;Residues: 1-9 <SHI>
C;Keywords: 91ycoprotein
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A:Molecule type: mRNA
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Titl. J. Cancer blockling analysis for malignant lymphoma and stomach cancer antigens fn
A:Reference number: AG035, WNID:990216080; PWID:2223853
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Cliff, Chim. Aria 207, 227-237, 1992
AFTILES: Partification and characterization of antigenic gitadins in comise disease.
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C:Date: 10-Dec-1995 %sequence_revision 08-Dec-1995 *text_change 08-Dec-1995
C:Accession: B66891
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C.Species Homo sapiens (man)
C.Date: 12-reb-127 sequence_revision 12-reb-1993 *text_change 17-Mar-1999
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            C:Keywords: qlycosidase: hydrolase: polysaccharide degradation
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                                                                                                                        DB 2;
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A.Molecule type: protein
A.Residues: 1-15 <SJO>
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while stiffs offer entry is copyright. It is produced though a collaboration between the Suiss institute of Bioinformatics and the EMEL outtration. The Bropeas individualities institute: "There are no restrictions on its modified and this striment is not; emone, these products of the contract a locate agreement (see by the concerned in the contract a locate agreement (see http://www.isb-sib.ch/nnnounce/or send an easil to ilcomestial-sib.ch/nnnounce/or send an easil to ilcomestial-sib.ch/nnnounce/
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COLINER'S E. Agolyuni A. Arcolina T.T., Baxter E., Blascoj R.G., A.,

Buschoff C., Chapser, A., Chowa C., Collotter L., Dyle C.N.,

Barchoff C., Chapser, A., Chowa C., Chowa M., Chelolita L., Dyle C.N.,

Baston R.A., Banasati S.W., Barta M., Machard M., Mith B., Nor B.,

Baston R.A., D. L., Domento M., Machard P., Mediredi M.,

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Pred, No. 7.2e+02;
1; Mismatches 1; Indels
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(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
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CLQA_RAT
CYSK_CLOPA
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NUEX_SOLTU
COW_CONVE
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Flygase; FBGn0028418; Leucokinin.
Neuropeptide; Amidation.
MOD_RES 15 15 15 AMIDATIO
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     STANDARD:
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Matches 5: Conserv
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                   January 28, 2003, 08:44:25 ; Search time 10 Seconds
(without alignment)
66.362 Willion cell updates/sec
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                         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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NO40_PEA
NO40_VICSA
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MAST_POLJA
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UR2B_CYPCA
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SMS1_MYOSC
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LPW_THETH
NO40_SESRO
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FIBA_MELME
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020A_CONTE
NO40_LOTJA
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Gapop 10.0 , Gapext 0.5
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Match Length D
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This SMISS proof merry is opergright. It is produced through a collaboration between the Suss institute of Holmionmatics and the EMEG contraction. The Burgeau informatic institute. These are no restrictions on its modified and this statement is notice moderned by the suspense of the statement is not removed. Base to provide the commercial moderned and the statement is not removed. Base to provide the commercial provides a license agreement (see http://www.isb-sib.cl/namounce/or send an easil to ilconseits-sib.cl).
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vinn Kamenn A., Bisselling T., Bisselling T., Verbords, Verbords, Verbords and Verbords
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 1; Length 13;
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Pred. No. 1.3e+03;
2; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE-96011756; PubMed-7548828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Matches 3; Conservative
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P55961;
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STRAIN-OF, Sparker IISSUE-Root nodules;
WREDIRES-55050611; pubMed-1948996;
MREDIRES-5006011; pubMed-1948996;
MREDIRES-FROM N., van de Sande K., Yang W.C., van Kammen A., Bisseling T.,
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France 17. 307
F
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Assignment of Borllius thermomyloliquedactens KP1071
alpha glucosidase 1 to an exc-alpha-1,4-glucosidase, and its striking
as familiarly to becalliary oil-of-logiousoisses in Neresinal sequence
and in structural parameters calculated from the maino acid
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Bikaryota, Viidiphantes Streptophyta; Embryophyta; Tracheophyta;
Bemtaropha, Mignollophyta; andlockyledons; core endicors; Rosidae;
eurosids I: Eabales; Fabaccae; Papilionoideae; Vicieae; Pisum.
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SAMILARITY).
- DEVELOREMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE MODULE
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11. ACTUTY - Hydrolysts of terminal, non-reducing 1.4-
11. ACTUTY - Hydrolysts of terminal, non-reducing 1.4-
11. ACTUTY - BESIDES WITH Falsess of D-91. HYDROL
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Pred. No. 7.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                               01-NOC-1992 (Rel. 23, Created)
01-NOC-1992 (Rel. 24) Last sequence update)
01-NOC-1992 (Rel. 24, Last annotation update)
MAIRSE (CS. 24. LOS) (Alpha-Licosidase I) (Frayment).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Barly nodulin 40.
                                                                                                                                                                                                                                                                                                                 15 AA.
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PIR; S21240; S21240.
Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T. Biochem, 205-249-256/1992)
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MEDLINE-92209510; PubMed-1555585;
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es 3; Conservative
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4 VLGKKOR 10
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1 MKKAWWKE 8
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5 VLWKKOK 11
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P55959;
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SEQUENCE
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Matches 3
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13-760-1787 (Res. O. Crested)
13-760-1787 (Res. O. Last sequence update)
13-760-1787 (Res. O. Last sequence update)
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13-760-1787 (Res. O. Crested)
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10. MGI 2022 (Rel. 20. Late update)
10. MGI 2022 (Rel. 20. Late update)
10. MGI 2022 (Rel. 202
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100.0%; Pred. No. 1.4e+03;
Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.4e+03;
ive 0; Mismatches 0; Indels
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NCBI_TaxID=31921;
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blakryota; Metanos Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Inseceta; Petryoton; Neopleta; Biodopetryota; Hymenopista; Apocrita;
Aculatai, Wespoldaa; Vespidae; Polistinae; Parapolybia.
                                                                                                                                                            Gaps
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The Targe 1996 (Mel. 31, Last sequence update)
16-07-200 (Mel. 40, Last Ennodation update)
16-07-200 (Mel. 40, Last Ennodation update)
Detail Advanced Mel Noplamerase beta (naham (FC 2.7.7.56) (Transcriptase beta 'chain) (MRA polymerase beta' chain)
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-!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma gallisepticum.
Agroplasma daturiouses; Mycoplasmataceae; Mycoplasma
NCBI TaxTiP 2096;
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Pred. No. 1.3e+03;
1; Mismatches 1; Indels
                                            Score 21, DB 1; Length 13;
Pred. No. 1.3e+03;
3; Mismatches 2; Indels
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Transferase; DNA-directed RNA polymerase; Transcription.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 M.
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                                            37.5%;
Ouery Match
Best Local Similarity 37.5%
3: Conservative
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STRAIN-A5969Var.B;
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-- FUNCTION: HA & A SUGGESTED ROLE IN OSNOREGULATION AND AS A CONTIONS. PROCESTED ROLE IN SMOOTH
-- CONTICOTROPIN-FELENSING FACTION. PROBABLY INVOLVED IN SMOOTH
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Piiseetskaya E.M., Andrews E.C., Gorban M.P.,
Kimmel J.E., Andrews E.C., Gorban M.P.,
Characterization of coho salmon (Oncorphynchus kisutch) islet
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Pred. No. 1.8e+03;
0; Mismatches 2;
16-OCT-2001 (Rel. 40, Last annotation update)
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Best Local Similarity
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01-NOV-1997 (Rel. 35, Last sequence update)
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last amnotation update)
Serine proteinase inhibitor (Fragment).
                                                                                                                                                                                                                                       01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
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Q10997;
                                                                                          MAST_VESBA
ID MAST_VESBA
AC P21654:
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scantostatin from the turlle, Pseudemys scripta.";
Peptides 11:46-466(1990).
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Tranchanys erripta (New cards sinder urtia) (Yesudanys scripta);
Bakaryota Metacon (Bordasa Cermisaa 'Werebreta' Buteleostomir,
Archosautra (Tocobylidae; Alligatorinae; Alligator;
                                        Control JA. Research C.F. Haston T. H. Hatter I. H. Thill in: 
Yearstortell related and pluosportraled peptides with unusual 
form. Comes. Documents from the Discopess self (Asbullla supplilla): '. 
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- SERICALINA SECRETION: SECRETION SPARITY.
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pred, No. 2.1e+03;
0; Mismatches 3; Indels
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Somatostatin-14.
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InterPro: IPR004250; Somatostatin.
Pfam: PF03002; Somatostatin: 1.
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MEDLINE-90341082; PubMed-1974347;
MEDLINE-89065329: pubMed-2904391:
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PIR; B60842; B60842.
PIR; A60840; A60840.
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Search completed: January 28, 2003, 08:54:00 Job time : 12 secs

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*Procrein database for several tissues derived from five instar slikworm.";
** Chuan Hsueh Pao 28:217-224(2001).
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Pred. No. 5.6e+02;
4; Mismatches 5; Indels
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MEDLINE-21177481; PubMed-11280994;
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01-NOV-1996 (TEMBLEL. 01, Created)
01-NOV-1996 (TEMBLEL. 01, Last sequence update)
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                       Best Local Similarity 35.7
Matches 5; Conservative
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SEQUENCE.
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score greater than or equal to the score of the result being printed,
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          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 16
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polests N. Kintre M. Higgehl Y. Yamada T.;
Tisolation and matho of Seepence of the 308 ribosomal protein S19
from Nycobecterium boxis RGC, "y
PERS Left. 319-914 (1987)
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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Pred. No. 2.5e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                   Score 25; DB 3; Length 15;
Pred. No. 2.4e+03;
5; Mismatches 1; Indels
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01.0A7-2000 (TEDBELGI 13. Created)
01.0A2-2001 (TEDBELGI 13. Lest empleme update)
CSA poptidase (Erapment) 15. Lest embestion update)
Elsea S.H., Haiung Y., Mitias J.L., Osheroff N.,
D. Boll. Chem. 270.1913-1920(1995).
SGD: SGDGGGG2; TOP2.
MAY-TRR 10.7
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NCBL_TaxID-1314;
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15 A5; 2094 NW;
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 40.0
Matches 4; Conservative
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WOOTON, W.F. MMIIIT., Wohkis M.L., Milmer P.G.; Tofentification of crook in persistences as well as the
"John-Hiller, and palesterophin, in human proteins, as well as the
Arterioseire." Throm. 113798-1805(1908) and posterior in the protein of the persistence of the John in Calebrance of the John 1379 MMI; Calebrance of the Campus Campus."
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Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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                                                                                                                                Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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45.5%; Pred. No. 1.1e+03;
Live 4; Mismatches 2; Indels
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pred. No. 1.7e+03;
1; Mismatches 0; Indels
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BRHL, HG36L9; AAAA24555.1; -1 1 1 1 1 1 1 SPBCA60581A4F3B CRC64; SPQUERCE 14 AA: 1705 WW; 7786CA60581A4F3B CRC64;
        01-NOV-1998 (TrEMBLrel, 08, Last annotation update)
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01-MAY-2000 (TERMBLEL 13, Last sequence update)
01-DEC-2001 (TERMBLEL 19, Last annotation update)
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Homo sapiens (Human).
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es 5; Conserv
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NCBI_TaxID=562;
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                                                   (Fragment)
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                                                                                                                                          061574, CARBELLEI, OV, CTERTON, CARBELLEI, OV, CTERTON, CARBELLEI, OV, CTERTON, CARBELLEI, OV, CTERTON, CARBELLEI, OV, STATE ABERDER, CHORACO, CHORALDEI, 15, Last annotation update)
Byperheita official recorded (Franchis
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Pred. No. 8.1e+03;
2; Mismatches 1; Indels
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PORÍGONIERI PA. O GENORAR B., Kistel A., Diugasseraka B.,
Namasada G., Graboska B., Kistel A., Diugasseraka B.,
Namasada G., Graboska B., Kistel A., Diugasseraka B.,
Sabantice G., Perin Juneza J.,
Sabantice G., Perin J. (1997) 11. 1. 1997, AMASIATA AMAS
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01-UUL-1997 (TrEMBLE). 04, Last sequence update)
01-NOV-1998 (TrEMBLE). 08, Last annotation update)
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01-DEC-2001 (TERBILE). 19, Created)
01-DEC-2001 (TERBILE). 19, Last sequence update)
01-DEC-2001 (TERBILE). 19, Last annotation update)
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Pred. No. 5.7e+03;
1; Mismatches 3;
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VASSIGNMENT OF BACKLINS THEOROGY/DOLINGEROGISSEs, AND LES SETEKING

SIMILARITY to Deciliary Oligo-i.s-q-luccolisase, and testriking

similarity to beciliary Oligo-i.s-q-luccolisases in *terminal sequence
and in structural parameters calculated from the amino acid

composition.
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01-MAY-2000 (TERBELFel, 13. Created)

01-MAY-2000 (TERBELFel, 13. Lats sequence update)

01-MAY-2000 (TERBELFel, 14. Lats annotation update)

TERTERPOORUM (TERBELFEL)

SERVENCE, VILIDIANTER, STEEPORYPER, EDITORIANTER, PROCESE, FORCESE, FORCES
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Pred. No. 5e+03;
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Pred. No. 5e+03;
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SEQUENCE 15 AA; 1931 MW; 6284CE40013D3042 CRC64;
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SEQUENCE 15 AA: 1742 MW; 285C8365ACC8832E CRC64;
                                  23.1%; Pred. No. 3.4e+03;
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MEDLINE-92209510: PubMed-1555585;
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Local Similarity 37.5%;
nes 3; Conservative
Best Local Similarity 23.1
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                                                                                                                                                                                                               2 LKEVLWKKQKDKV 14
                                                                                                                                                                                                                                                                                                                                   3 TOOLVRKGRRDKI 15
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6 PSGQVQWPQ0 15
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Packrode C. IIII. Keela J.W.:
"Mapping of Expressed Sequence Tags from a porcine early embryonic companies, the processed Sequence Tags from a porcine early embryonic Submitted (MAY-2000) to the DeWil. Med.788 AAG2593.13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Punctional amoration of a full-length mouse cDNA collection."; where 40:865-690(2001).

*Punctional Amountain Amoun
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Pred. No. 1.1e+04;
1: Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                     Length 15;
                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                        SEQUENCE 15 AA: 1825 MW: P9FFE0E30FDB921E CRC64:
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101-1019-2001 (TERBATCAI. 17, Created)
101-1019-2001 (TERBATCAI. 17, Created)
101-1019-2001 (TERBATCAI. 17, LABS SEQUENCE update)
101-1019-2001 (TERBATCAI. 17, LABS SEQUENCE update)
101-1019-2001 (TERBATCAI. 17, LABS SECONDESIDE)
101-1019-2001 (TERBATCAI. 17, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 AA: 1881 MW: 029ECFC9BC205263 CRC64:
                                                                                                                                                                                                                                                                                                              Score 21; DB 6;
Pred. No. 1e+04;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA
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01-NAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 VLWKKOKDK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VVHMKOKGK 14
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                                                                                                                                                                                                                                                                       SEGURNER PROF. N. A. WEDLINE-9756G121; Phubed-9106215; Phum G., COLF. F., "Pubed-9106215; Phum G., COLF. F., "Studies on prolysostaphin processing and characterization of the "Studies on prolysostaphin memority factor (Liff) of Staphylococcus simulans biovar stephylolyticus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4MY-2000 (TERMBLrel. 13, Created)
0.4MY-2000 (TERMBLrel. 13, Last sequence update)
0.4MY-2000 (TERMBLrel. 14, Last annotation update)
Valine sensitive acetolactate synthase large subunit (EC 4.1.3.18)
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01-MR-2001 (TEMBELEL, 16, Last enconstaton update)
63-Mpc-Lin 1joht (baharilke protein (Fragment),
83-Mpc-Cin (Pig),
83-Mpc-Cin (Pig),
83-Mpc-Cin (Pig),
83-Mpc-Cin (Pig),
84-Mpc-Lin (Pig-Cin (Pig),
85-Mpc-Cin (Pig),
85-Mp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                              (Fragment).
Staphylococcus simulans.
Bacteria; Firmicutes: Bacillus/Clostridium group; Bacillales;
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MELLED-31281(0); DANAG-450763).
MELLED-31281(0); DANAG-450763).
POLICICALION and Obseroterization of the value semsitive functioning or section of the profits an excessor AND 25419.'; accordance of the NEW 11871(1981).

REPUBLISHED TO SERVICE OF THE STATE 
Similar to bin3 and sin recombinases of Staphylococcus aureus
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Pred. No. 1e+04,
1, Mismatches 2, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 2; Length 15;
Pred. No. 1e+04;
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SEQUENCE PROM N.A.
Smith T.P.L., Fahrenkrug S.C., Rohter G.A., Simmen F.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA: 1808 MW: 1D1A4AB1RE1E3CFF CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23:1251-1265(1997).
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EMBL: U66883; AAB53786.1; -.
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Best Local Similarity 50.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KEVLWKKOKDKV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ROTVYSINKDRV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                          Staphylococcus.
NCBI_TaxID=1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBC_TaxID=9823;
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NCBI_TaxID=615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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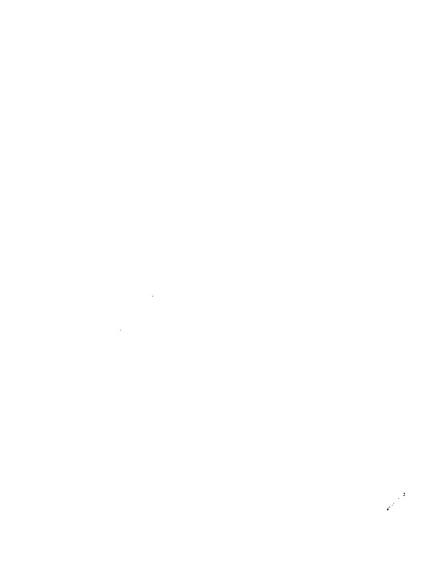
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The invention criticals to separative perpetuiting series and their corresponding the highest ordered and sething from the contractility, nutrient prefets, growth homenon, series than of the contractility, nutrient to the sequence of the invention are used as and homenon. The sequence of the invention are used in the prevention, distincts as the motifier claim of the contraction and their complements are used as the production of their complements are used as the production of analysis of the contraction and their complements are used as the production of analysis of the contraction of analysis of the contraction of analysis of the production of analysis of the contraction are used to condition analysis of the process and notice colds of the invention are used to conditions again to end process and process. The page of the process and process and analysis of the process and anyther or analysis of the process and anyther or analysis 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inferent sign31-like pepticle; SISINF, immunity; developmental, process; inferent human imminodeficiency virus; veccine; anthypoglycemic; adsorption onhoner; pastrointential, disease; prove incline and pastrointential, disease; growth related disease; admention; gene therapy; growth regulation; blood wessel formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptides, useful for modulating gastric contractility, niptake, pancreatic secretion of hormones, digestive enzymes and treating gastrointestinal and growth related diseases, comprises seig3:like peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 23; Length 16;
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deisher TA, Bishop PD;
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     digestive/pancreatic enzymes and hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٤
                                                    Claim 5; Page 30; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE15891 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human zsig33-gamma peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-2000: 2000US-0569271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV; 281933-gamma peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (2YMO) SYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LKEVLWKKQKDKVAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LODILWEEAKEAPAD 16
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB: AAD25764.
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2SIG33-Like peptides and polynucleotides, useful for modulating gastric contractlity, nutrient uptake, growth hormones and/or secretion of digestive/pencreatic enzymes and hormones -
                                                                                                                                                            The invention relates to zsig33-like peptides and their corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; z81g33-like peptide; gastric contractility; nutrient uptake;
growth hormone digestive enzyme; restorative therapy; gene therapy;
protein therapy; gastrointestinal; endocrine; anabolic.
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Pred. No. 76;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE23847 standard; peptide; 16 AA
                                                                                                   Claim 5; Page 30; 34pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 33.3
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
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(SHEP/) SHEPPARD P O.
(DEIS/) DEISHER T A.
(BISH/) BISHOP P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LODILWEEAKEAPAD
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The invention rathers to stagin-like spetial (SISIR), intelluding the first intelluding stagin-like period (SISIR), intelluding she stagin-repeated stagin-rep
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                                                                                                                                                                                                              New polypeptides, useful for modulating gastric contractility, nutrient uptake, plancreatic secretion of hormones, digestive enzymes and treating gastrocintestinal and growth related diseases, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bovine small piroplasma protozoa; 33 kDa protein; vaccine;
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                                                              Bishop PD:
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                                                        Deisher TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragment of T. sergenti 33 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                    Claim 5c; Page 85; 89pp; English.
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                                                              Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
(ZYMO ) ZYMOGENETICS INC.
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                                                                                                                      MPI: 2002-082982/11.
                                                                                                                                                                                                                                                                                                            zsiq33-like peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5, Conserva
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                                                                                                                                                      N-PSDB: AAD25764
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Pred, No. 76;
7; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE15892 standard; peptide; 16 AA.
                               Claim 5b; Page 85; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human zsig33-gamma peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 AA;
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The invention of altering macronic decides for prometing nearest varieties of a consolidate state of the consolidate 
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growth hormone; digestive enzyme; restorative therapy; gene therapy;
protein hierapy; gastrointestinal; endoctine; enabolic.
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0; Mismatches
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85.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE23848 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human 2S1933-gamma peptide #4.
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(DRIS/) DEISHER T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JASP/) JASPERS S R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences (NTSs),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 WKKQKRK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2002055156-Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a fragment of the principal 33 Mba protein of a region (see also 87394). T. sequent is a bodie assall piroplasm proceso. This sequence contains the MRK sequence which is the smallest proceso. This sequence contains the MRK sequence which is the smallest warmonestic unit of the 33 Mba protein. This protein can be used in a veaccine for prevention of boulne small piroplasm disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                              New bovine small piroplasma protozoa peptide(s) · contg. the Lys-Glu-Lys sequence, used for preventing infection or detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                         Mivahara 7;
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le+02;
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                                                                                                                                                                                         Kawazu S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                        KAGA ) CHEMO SERO THERAPEUTIC RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35;
Pred. No.
                                                                                                                                                                                                                 Taneno A, Yamada
                                                                                                                                                                                         Kashiwazaki M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY69683 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 16; 20pp; English.
                                                                                                                NORQ ) NAT INST ANIMAL HEALTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.7%;
                                                                    43.TD-0238864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US12126.
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                   94AU-0070373.
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Best Local Similarity 55.6'
Matches 5: Conservative
                                                                                                                                                                                         , Kamio T,
Sakai E, 1
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                                                                                                                                                                                                                                                             WPT: 1995-147719/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ] EVVWKEKKE
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23-OCT-1998;
                   22-AIG-1994:
                                                                    30-AIG-1993:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1999;
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                                                                                                                                                                                         Fullsaki K,
                                                                                                                                                                                                             Nonaka F.
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                   4 X E X E E X E
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the invention contains to say 13-11th popular (18319), including a say 11-11ther, say 13-11th popular and more says 11-11ther, say 13-14th popular and more says 11-11ther. Say 13-14th popular and more says 11-11ther. Say 13-14th popular says 13-14th popular says 11-14th popular say
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                                                                                                                                                                                                                                                                                       New polypoptides, useful for modulating sparkit contractility, nutrient types. Perfect programming a spartner for the first programming and growth related diseases, comprises first particulations.
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Pred. No. 1.4e+02;
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                                                                                                                                       Deisher TA. Bishop PD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM98523 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5d; Page 85; 89pp; English.
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                                                                                                                                       Jaspers SR, Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-2002 (first entry)
                                                  (2YMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                    WPI: 2002-082982/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM98523:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relative to satisfaction and the contracting the prevention of purely, ground because and amount of purely, ground because and amount of purely, ground because and because at the sequence of the invention are used in the prevention, disponsis and the sequence of the invention are used in the prevention, disponsis and the sequence of the invention are used in the prevention, disponsis and the medical cand of the invention are used as an used as one of manner invention of the face of the invention are used as the prevention of sharing the presence of a manner invention of the purely of the prevention of the prevention of the prevention of an invention are used to contain a sequence of the invention are used on a season of the presence of SESI31 expression and settivity. The anti-SESI3 anti-Delies and an anogeneous and settivity. The presence of SESI31 in sequence of the presence of SESI31 in sequence of the invention are used to complain a sequence of the invention are used to see the sequence of the invention are used to see the sequence of the invention are used to see the sequence of the invention are used to see the sequence of the 
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                                                                                                                                                                                                                                                     2SIG33-Like peptides and polynucleotides, useful for modulating gastric
contractility, nutrient uptake, growth hormones and/or secretion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mman; saig33-11ke peptide; 8331D; immunity; developmental process; infection; human immodeficiency vites; vectices unityposlypemanic; adaptption enhance; gestichicestival disease; growth related disease; srowth related disease; strowth related disease.
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                                                                                    Jaspers SR, Sheppard PO, Deisher TA, Bishop PD:
                                                                                                                                                                                                                                                                                                                                          114estive/pancreatic enzymes and hormones -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE15893 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 30; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human zsig33-gamma peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2001; 2001WO-US15091.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 35.17
57 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LKEVLWKKORDKVA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LODILWEEAKEAPA 15
                                                                                                                                                                 WPI: 2002-443750/47.
(BISHA) BISHOP P. D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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AAE15893
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the mann purpoportures I (rept) has fore comen alleds posts and posts the set of the set
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coronary heart failure; directic therepy; thistolic loop diuretic:
water diuresis; congestive heart failure; liver cirriposis;
empirolic agodices; hypostalemis; cedema; antique;
acute renal failure; hypostalemis; cedema; antique;
                                                                                                                                                                                                                        Test processes for detecting polymorphisms - useful for identifying alleles of human gene encoding phospho-glucomutase-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 15; Length 16;
pred, No. 3e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harlow KW;
                                                                                                                                                                                                                                                                                                                                                               Disclosure; Table 5, page 12; 42pp; English
                                                                                       Whitehouse DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nociceptin-like immunogenic peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petersen JS, Kapusta DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU76075 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.1%;
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05-OCT-2000; 2000DK-0001485.
06-DEC-2000; 2000US-251671P.
13-JUN-2001; 2001MO-US41008.
                           (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L5-JUN-2001; 2001WO-US19113
                                                                                              Edwards YH. Hopkinson DA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.1
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZEAL-) ZEALAND PHARM AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LKEVLWKKQKDK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 MKEAIOKKKKK 15
                                                                                                                                                           WPT: 1994-341885/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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а
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concoling polymorphic variants of procisins related to anylases, anyloid
processar, anialgopiestim, apportant scaled southernia, caleful, occini,
considerable of the control of the control occinion occinion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogners and histories, useful for inapprosing and treating, e.g. encer, autoimmune diseases and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32, DB 22; Length 14;
Pred. No. 2.78+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pair 3 Pep 5 immunogen for human PGM1 isozyme allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 4062; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR66027 standard; Protein; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.1%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                    28-DEC-2000; 2000WO-US35498
                                                                                                                                                                                                                                                                 28-DEC-1999; 99US-0173419.
27-DEC-2000; 2000US-0173419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Leach M;
                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AA:
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                                                            40200147944-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-1994;
Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1993;
                                                                                                                                05-JUL-2001.
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M. The threading makes to a propriet copying to the greenist (A).

A. L. 1-X-Z. - Z. (A), where X - a imanagation of formula (B);

A. L. 1-X-Z. - Z. (A), where X - a imanagation of formula (B);

A. L. 1-X-Z. - Z. (A), where X - a imanagation of formula (B);

A. L. 1-X-Z. - Z. (A), where X - a imanagation of the formula (B);

A. L. 1-X-Z. - Z. (A), where X - a imanagation of the formula (B);

B. L. 1-X-Z. - Z. (A), which is a provided that fore including the control of the formula (B);

B. J. 2-X-Z. (A), which is a provided that fore including the control of the formula (B);

B. J. 2-X-Z. (A), which is a provided that fore including the control of the formula (B);

A. T. 2-X-Z. (A), which is a provided that fore including the control of the formula (B);

A. L. 1-X-Z. (A), which is a provided that fore including the control of the contr
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                                                                                                                                                                                                                     New peptide conjugate useful for preparing medicament for treating congestive heart failure. I liver offribols; a pehicolic syndrome and hypertension comprises modified N and/or cerminals
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Pred, No. 7.8e+05;
1; Mismatches 1; Indels
                                                                                                                                                                 Harlow KW:
                                                                                                                                                                 Petersen JS, Kapusta DR,
                                                                                                                                                                                                                                                                                Disclosure; Page 7; 72pp; English.
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                                                                                    2000US-251671P.
2001WO-US41008
                                15-JUN-2001: 2001WO-US19113.
                                                          L6-JUN-2000; 2000DK-0000944
                                                                         2000DK-0001485
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                                                                                                                                (ZEAL-) ZEALAND PHARM AS.
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Best Local Similarity
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                                                                                    06-DEC-2000;
                                                                         05-OCT-2000;
                                                                                                                                                                 Jarsen BD,
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                                      New peptide conjugate useful for preparing medicament for treating congestive heart failure. Liver citriosis, nephrotic syndrome and hypertension comprises modified N and/or C terminals
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coronary heart failure duretic therepy thatactie; loop duretic;
water dureasis; congestive heart failure; liver cirricasis;
empiractic spardome; hypostalemia; occema; antigen failure;
acute renal failure; hypostalemia; occema; antigen failure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.9%; Score 31; DB 23; Length 8; 71.4%; Pred. No. 7.8e+05; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nociceptin-like immunogenic peptide #3.
                                                                                                   Disclosure; Page 7; 72pp; English.
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Best Local Similarity
5; Conserva
           WPI; 2002-171551/22.
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The intension calculate to appelle conjugate of the general (challe (A))

R. 1-3-22-12 (A); where X = a heappelled of formula (B);

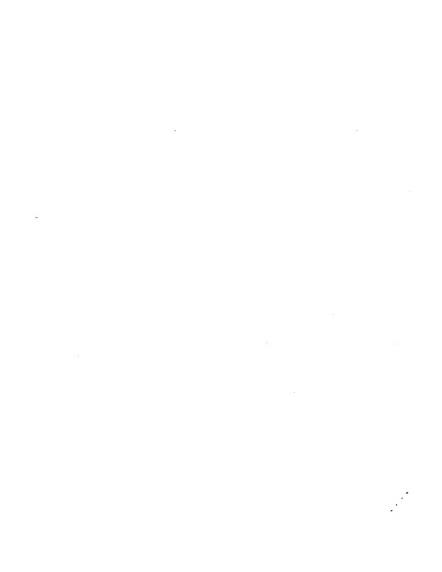
R. 1-3-22-12 (A); where X = a heappelled of formula (B);

R. 20 and 10-22-12 (A); where X = a heappelled of formula (B);

R. 20 and 10-22-12 (A); where X = a heappelled of formula (B);

R. 20 and 10-22-12 (A); where X = a heappelled of the third of a calculate of the conjugate of the prevention of the conjugate of the conjugate of the prevention of
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                            /note- "Arg is acetylated"
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/note= "Lys is amidated"
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36-DEC-2000; 2000US-251671P.
13-JUN-2001; 2001WO-US41008.
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Best Local Similarity 71.4*
"...e 5; Conservative
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    Wodified-site
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06-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compositions comprising nucleic acid condensates having a nucleic acid
bound to two low molecular weight cationic linkers, used in human gene
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                                               Nucleic acid condensate; cationic linker; gene therapy.
Amino acid sequence of a cross-linking peptide.
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therapy, and diagnostics -
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Best Local Similarity
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                                                                                              Synthetic.
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concoary heart failure. The beampeptides are in part based on the sequence of formula (RK)Y(RK)(RK) a partial agonist of the nocitosptim, opioid receptin, opioid receptor-like one (PKL) which can be used to raise antibodies against the complates. The present sequence is a peptide conjugate of the invention.
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Pred. No. 3.3e+02;
1; Mismatches 1; Indels
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Job time : 36 secs
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                                                                                                                                                                                                                                                                5: Conservative
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                              12 AA;
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preferably (14 200. ct. 25 200. ct. 10. 82.7. master of tale Also 
preferably (14 200. ct. 25 200. ct. 3 20.7. master of clatte Also 
included are motate acids encoding the peptides. a heat cell comprising. 
The peptides and conjugates are useful for the preparation of a 
medicinent for the treatment and/or prevention of proparation of a 
preferably sacciated with heart failure, or with intensive diuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a peptide conjugate of the general formula (A).
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                         AAU76099 standard; peptide; 12 AA.
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05-OCT-2000, 2000bk-0001485,
06-DEC-2000; 2000uS-251671P,
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                                                                                                                                (first entry)
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AAU76099
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sequence 4, App II sequence 4, App II sequence 1, App II sequence 124, App II sequence 134, App II sequence 119, App Sequence 119, App Sequence 119, App Sequence 115, App Sequence 2, App II sequence 3, App II sequence 3, App II sequence 3, App II sequence 2, App II sequence 3, App II sequence 9, App II sequence 11, App Sequence
Sequence 3, Appli
Sequence 26, Appl
Sequence 48, Appl
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8.1;
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Sequence 15. Application Us/0965323

Perent No. USGADO05553501

Perent No. USGADO055501

Perent No. USGADO05501

Perent No. USGADO05501
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Pred. No. 8
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APPLICANT: DETSHER THERESA
APPLICANT: BISHOP, PAUL
TITLE OF INVENTION: 284933-11ke Peptides
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US-09-863-253-16

Sequence 16, Application US/09853253

Patent No. US20020055156A1

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.9
Best Local Similarity 33.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: JASPERS, STEPHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LKEVLWKKQKDKVAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LQDILWEEAKEAPAD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-853-253-15
     RESULT 1
US-09-853-253-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 16
PRT
sequence 1), April Sequence 10, April Sequence 10, April Sequence 2, April Sequence 3, April Sequence 4, April March Sequence 4, April March Sequence 4, April March Sequence 5, April Sequence 3, April Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                  January 28, 2003, 08:54:40 ; Search time 11 Seconds
(without alignment) 29:351 Willion cell updates/sec
29:351 Willion cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pott Island, Uppil Lotton & M.; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999; 1999
                               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122226 seqs, 20178551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                                                           US-09-730-465-2_COPY_50_65
                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                               1 PLKEVLWKKQKDKVAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                   OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
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35.7%; Score 30; DB 10; Length 9; 66.7%; Pred, No. 1e+05; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                               SOFWHARE PATENTIN RELEASE 11.0. Version #1.25
CURRENT APLICATION NOWER: 05/09/881.490
FRING APPLICATION NOWER: 14-200-2001
PRING APPLICATION NOWER: 14-200-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /label- D-Amino Acids
/note= "Positions 1-9 are D-amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: C-Terminus
OTHER INFORMATION: /label Amidation
/note The C-Terminus is Amidated
                                                                              COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAPACION COMPANY OF A THROUGH O
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/119,858
FILIND DATE: -GINKEROM-
PALLCATION NUMBER: 08/372,105
APLICATION NUMBER: 08/306,473
APLICATION NUMBER: 08/306,473
APLICATION NUMBER: 08/305,430
                                                                                                                                   COMPUTER REACHER FORM:
MEDIUM TYPE: TLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 163
US-09-881-490-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE 3.12.707-9155
TELEPHONE 3.12.707-9155
TELEKK: 312.707-9155
TELEKK: 503 388 1.248
TELEKK: 503 388 1.248
TELEKK: 15 308 1.248
TELEKK: 15 308 1.248
TELEKK: 9 amilto acid
TOPOLOGY: 1inear
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Patent No. US20020006638Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.77
Matches 4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 EVLWKK 9
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US-09-765-527-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.9%; Score 36; DB 10; Length 16; 33.3%; Pred. No. 8.1; Live 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.5%; Score 34; DB 10; Length 15; 35.7%; Pred, No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th FloorDrive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fadem Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES, 211
CORRESPONDENCE ADDRESS:
CITE STRUMENTO. 00-30
CITERENT NOLICENTON WHORRE: US/09/651.253
CITERENT TAILOR DATE: 2001-105-10 / CITERENT TAILOR DATE: 2001-105-10 / CITERENT TAILOR MANERS: 60/203-300
NUMBER OF SEXU TO MASS: 2007-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17. APPLICATION 18.709833253
PROGENEAL INFORDITATION 18.709833253
PROGENEAL INFORDITATION 18.709833353
PROGENEAL INFORMATION:
APPLICAMT GREENEAL THRESA
APPLICAMT BERENEAL THRESA
APPLICAMT BERSEON 19.709
PLIE REPERENCE: 00.700
PLIE REPERENCE: 00.700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION WUMBER: US/09/953,253
CURRENT FILING DATE: 2010-05-10
FRIOR APPLICATION NUMBER: 60/203,300
FRIOR FILING DAME: 2000-05-11
NUMBER OF SED ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 163, Application US/09881490
Patent No. US20020077298AL
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Little II, Roger G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lim, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33.3%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LKEVLWKKOKDKVAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LODILWEEAKEAPAD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LKEVLWKKQKDKVA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LODILWEEAKEAPA 15
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (16)...(16)
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1. LOCATION: (15)...(15)
US-09-853-253-17
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Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-881-490-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-853-253-17
                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                             LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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0; Gaps 0;

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Segmenter 57, April 1941 to 18/9984036
PRICAR NO. 1922(00)21000A1
PRICAR NO. 1922(00)21000A2
PRICAR NO. 1922(00)21000A2
PRICAR NO. 1922(00)21000A2
PRICAR NO. 1922(00)2100A2
PRICAR NO. 1922(00)210A2
PRICAR NO. 1922(00)222
PRICAR NO. 1922(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.0%; Score 26; DB 10; Length 9; 50.0%; Pred. No. 1e+05; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      023070-086100US
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REOF PLIAN DER 2001.07-199
REOF PLIAN DER 2001.07-199
REOF PLIAN DER 2001.07-19
REOF PLIAN DER 2001.07-17
REOF RELIEM DER 2001.07-17
REOF RELIEM DER 2001.07-17
REOF RELIEM DER 2001.07-17
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RED 2001.07-
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FILING DATE: 01-MAY-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                      COMPUTER REDUALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PC-EOFILE Release #1 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME AND THE STATE OF THE STATE OF THE STATE OF THE STATE OF ADMINISTRATION AND THE STATE OF THE
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US-09-071-838-74
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ORCANISM: Homo sapiens
US-09-984-056-85
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Best Local Similarity
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SEQ ID NO 85
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CLASSIFICATION:
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APPLICANT: Better, Marc D.
TITLE OF INVENTION: Wethods for Recombinant Microbial Production of NUMBER OF SEQUENCES: 265
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
STABLIL O'TOOLE, Gerstein, Murray & Borun
RDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6500 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB 10; Length 15;
Pred. No. 88;
1; Mismatches 2; Indels
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APRICANT Klyose, Temblic Personal APRICANT Adeach Remin
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CURRENT APPLICATION DATA:
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COTER IMPORATION: Thebal Amidation
COTER IMPORATION: Thebal Amidation
SERVICE DESCRIPTION: SEQ ID NO: 101:
US-09-76-527-101
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REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
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OTHER INFORMATION: "XMP.I20"
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
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Patent No. US20020152501A1
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 101:
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Best Local Similarity 62.5%;
Matches 5: Conservative 1
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APPLICANT: Fische
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5 KKHKDK 10

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CORRESPONDENCE ADDRESS:
ADDRESSE: FIRE SCRIPPS RESEARCH INSTITUTE
STREET: 10666 No. US20020013456Alth Torrey Pines Road, TPC-8
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ADDRESSER: THE SCRIPPS RESEARCH INSTITUTE
STREET: 1066 No. 10220020133000Alth Torrey Pines Road, TPC-8
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ODBUTER READABLE FORM:
MEDINY TERE FLOOPULEN,
ODBUTER STREET,
ODBU
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APPLICANT OF COCCESS LISTS
SINGLES COCCESS RESIDENCE
HARTEN COCCESSARY IN NUMBER TIDES.
TITLE OF INVENTION: COMPOSITIONS AND METRORS
COMPOSITIONS AND METRORS.
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REGISTRATION NUMBER: 31,796
REGISTRATION NUMBER: 23,796-0002
TELEPONNI INTOVATION INTOVATION:
TELEPONNI (413) 324-0038
TELEPON (413) 324-0038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/766.396
FILING DATE: 18-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/857,389
FILING ATTE: <URANOWAN
ATTORNEY/AGBNT INFORMATION:
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US-09-766-396-8
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US-09-766-396-8
; Sequence 8. Application US/09766396
; Patent No. US2002003456Al
; GENERAL INFORMATION:
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TYPE: amino acid
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FRAGMENT TYPE: C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SROITENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
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55.6%; Pred. No. 1.8e+02;
tive 1; Mismatches 3; Indels
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                           US-09-984-057-85
: Sequence 85, Application US/09984057
; Patent No. US20020151677A1
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Best Local Similarity 55.69
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5: Conservative
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US-09-984-057-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo Sapiens
US-09-791-378-302
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 VLWKKOKDK 13
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5 KKHKDK 10
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CITY: La Jolla STATE: California

RESULT 10

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APPLICANT: Wilson, Carol.

APPLICANT: See, Suprond
APPLICANT: See, Suprond
APPLICANT: To Hishlift, CELFELLE
APPLICANT: To Hishlift, CELFELLE
APPLICANT: To Hishlift, CELFELLE
APPLICANT: A Hishlift Compounds and Methods For Identifying Binding Compound
THIRD SEPECTANTION WINNER: 1501-15-35
PROTE RELEATION WHERE: 1501-15-35
PROTE RELEATION WHERE: 1501-15-35
PROTE RELEATION WHERE: 2001-15-32.
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50.0%; Pred, No. 2.5e+02;
Live 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Small peptide liquand binding compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEUROPEPTIDES,
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REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 22908-0002
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-766-396-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-03-21
PRIOR PELCATION NUMBER: US 60/191,299
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ. ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CORTISTATIN:
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de Lecea, Luis
Siggins, George R.
Henriksen, Steven J.
                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-7041
TELEFAX: (415) 324-0638
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/10062375
Patent No. US20020133000A1
GENERAL INFORMATION:
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Patent No. US20020064770A1
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
FRAGWRNT TYPE: C-terminal
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                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.07
Matches 4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nestor, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KEVLWKKOKDKVA 15
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ADDRESSE: THE SCHEPE RESEARCH INSTITUTE
STREET: 1056 No. US20020013455Alth Torrey Pines Road, TPC-8
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                                                                                            MEDIAN TIPE: Floppy disk CompuTRS: Ploppy di
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COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 22908-0002
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FILING DATE: 18-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/062,375
FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/857,389
FILING DATE: <Unknown>
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/857,389
FILING DATE: «IORNOWD ATTONEY/AGENT INFORMATION:
NAME: Schmonsees, William
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FRAGMENT TYPE: C-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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de Lecea, Luis
Sigglis, George R.
Henriksen, Stewen J.

TITLE OF INVENTION: CORTISTATIN:
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TELEPHONE: (415) 324-7041
TELEFAX: (415) 324-0638
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/09766396
Patent No. US20020013456A1
GENERAL INFORMATION:
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NAME: Schmonsees, Will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                               COMPUTER READABLE FORM:
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STATE: California
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Best Local Similarity 50.09
Matches 4; Conservative
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COUNTRY: US
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8 PNRRMKWKK 16

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Search completed: January 28, 2003, 08:58:42
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NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10666 No. US20020133000ALEh TOTTERY PINSE ROAd, 7PC-8
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No. 2.7e+02; Matches, 4; Conservative 2; Mismatches 3; Indels Matches 4; Conservative 2; Mismatches 3; Indels
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US-09-981-286A-4
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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STATE: California
COUNTRY: US
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2 PCKNFFWK 9
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US-09-981-286A-4
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Sequence 11, Appl.
Sequence 11, Appl.
Sequence 11, Appl.
Sequence 21, Appl.
Sequence 35, Appl.
Sequence 35, Appl.
Sequence 35, Appl.
Sequence 37, Appl.
Sequence 47, Appl.
Sequence 66, Appl.
Sequence 86, Ap
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PREMER NO. 185441

PREMER NO. 185441

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rice, Kevin G.
APPLICANT: Wadhwa, Manpreet S.
TITLE OF INVENTION: Peptides for Gene Delivery
NUMBER OF SEQUENCES: 11
105-00 e559-044-0
105-00 e559-044-1
105-00 e559-
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STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/237,309
FILING DATE: 26-AUG-1988
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FILING DATE: 30-MAR-1998
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Sequence 5, Application US/09050811
Patent No. 6387700
GENERAL INFORMATION:
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NEDIUM TYPE: Floppy disk
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WKKQKDK 7
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5185441-12
         Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                       January 28, 2003, 08:53:06; Search time 34 Seconds (without alignments) 13:846 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1100%
Listing first 45 summaries
                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
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84
1 PLKEVLAKKOKDKVAE 16
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Score Match Length DB
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Maximum DB seq length: 16

    COURT AND COURT COU
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Perfect score;
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                                                                                            Score 31; DB 4; Length 15;
Pred. No. 95;
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                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OFREATING SISTEM: PC-TOGS/MS-DOS
SOFTWARE: Patenfar Restease #1.0, Version #1.30
SIGNERN APPLICATION DAYA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APTICANT SIGNATURE (SERVIN C. APTICANT)
APTICANT: Wednew. Monthew. Monthew.
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Patent No. 1898974
APRICONT: Little 11. Roger G
APRICONT: Little 11. Roger G
APRICONT: ARICHMENTOR! B
TITLE OF INVESTOR! ARIL-Ungel Peptides
OWERSEO SOURCES: 10.
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                                                                                                                                                                                1: Mismatches
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FILING DATE: 30-MAR-1998
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NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09050811
Patent No. 6387700
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TELERAX: 415/397-8338
INFORMATION FOR SEQ. ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                                            Query Match 36.9%;
Best Local Similarity 71.4%;
Matches 5: Conservative
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MEDIUM TYPE: Floody
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STRANDEDNESS: not
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US-08-621-259A-205
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                us-09-050-811-6
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OTHER INFORMATION: position is bound to an Alkaloid by a Sulfide."
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ORBERTAINS SENSIBLE PC-00S/MS-00S

ORPHANE: PAINTING SENSIBLE AND UNIVERSED 11.30

CHRENE PAINTING NATA.

PRILIAN ORDINGER: US/O9/050,811

FILING DATE: 109-0051

CLASSIFICATION: 514
                                                                                            UM-03314
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NAME: CAITOL, Peter G.
REJETRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UN-03314
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32.837
REPERRNCE/DOCKET NUMBER: UM-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
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TELEPHONE: 415/705-8410
TELEFAK: 415/397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
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STRANDEDNESS: not relevant
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MEDIUM TYPE: Floppy
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OTHER INFORMATION: /note= "Positions 1-9 are D-amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARPHICANT, MARINEMION: ANIL-Yungal Peptides MARMAGEN OF SUNDERS: 2002 SUNDERS: 2002 OCCUPATION OF SUNDERSEE. MARTANI: 070016, Generalm, MARTAN & BOTUM STREET: 6100 Sears Tower, 213 South Wacker Dilve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label- Amidation
OTHER INFORMATION: /noce- "The C-Terminus is Amidated.
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COMPATTING STEPRING PACCOMMENTING TO COMMENTING STEPRING PACCOMMENTING STEPRING PACCOMMENTING STEPRING PACCOMMENTING PACCOMMENT 
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
PCT-1035-09262-163
PCT-1039-09262-163
; Sequence 163, Application PC/TUS9509262
; GENERAL INFORMATION:
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STATE: Illinois
COUNTRY: United States of America
2IP: 6060-6402
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 13-JAN-95
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.332"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 OILWKK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-621-259A-163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRATITEE.
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OTHER INFORMATION: /note= "Positions I-8 are D-Amino Acids."
US-08-521-2594-205
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LOCATION: C-Terminus
OTHER INPORMATION: /label- Amidation
OTHER INPORMATION: /note- "The C-Terminus is Amidated,"
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                                                                                                                                                                                                                                                                                         MENDION TYPE: FORPY GLAR.

COMPUTER: 100 HC Compatible 08

APPLICATION NUMBER: 08/204 811

APPLICATION NUMBER: 08/204 811

APPLICATION NUMBER: 08/204 811

APPLICATION NUMBER: 08/204 811

TREADMENT ADDRESS: 200 HC COMPATIBLE 08/204

TREADMENT ADDRESS: 200 HC COMPATIBLE 08/204

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APPLICANT: Little II, Roger G
APPLICANT: Little Edward
APPLICANT: Little Fadem, Mitchell B.
TITLE OF INVENTION: Arti-Fungal Poptides
NUMBER OF SEQUENCES: 252
CORRESPONDEME: ADDRESS:
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                                                                                                            STATE: Illinois
COUNTRY: United States of America
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Patent No. 5858974
                                    500 West Madison Street
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LOCATION: 1-8
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LENGTH: 8 amino acids
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                                                                        Chicago
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APPLICANT: Brownell. Riles
APPLICANT: Brownell. Riles
APPLICANT: Grownell. Riles
TITLE OF NUMBRICH: Cylcolor Lyuphocyte Antigen 68 o
THIR OF NUMBRICH: Cylcolor Cylcolor Forcesse Inhibitor
CORRESPONDER: ADDRESS: 1
CAPPETER REPAIRE FORM:
MEDIUM TYPE: FLOPPY CLAS.
COMPUTES: IRM COMPACTION
OF STATEMENT STATEMENT FOR STATEMENT
OF STATEMENT STATEMENT FOR STATEMENT STATEMEN
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COMPUTER: IN PF COMPATIBLE OF ORDER OF STEER) FOR COMPATIBLE OF COMPATIBLE OF ORDER OF OR
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APPLICATION NUMBER: US 08/373,215
FILIAGO DAY: 18 MAY-1995
APPLICATION NUMBER: US 08/37/05532
APPLICATION NUMBER: US 08/37/05532
PRIOR APPLICATION DAY.
FILIAGO DAYE: 13-70L-1993
FILIAGO DAYE: 17-70L-1993
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STREET: 10 S. Wacker Drive Suite 3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REPERENCE/DOCKET NUMBER: SCR1119P
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; Sequence 11, Application US/08485937
; Patent No. 5962633
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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Best Local Similarity 55.6
Matches 5; Conservative
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TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-907-190-13
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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LOCATION: 19
OTHER INFORMATION: //Albel- D-Maino Acids
OTHER INFORMATION: //note- "Positions 1-9 are D-amino acids"
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| LOANTON: C-Termins | COTHER INFORMATION: / Anidated | COTHER INFORMATION: / Anide-"The C-Termins is Amidated | PCT-1895-1985-148
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TLIANG DARKE, 11-14AR-91
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PREDICATION MURREL. 067439,722
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                                                                                                                                                                                APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
           APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
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TELEFX: 25-3856
TROMATION POS SEQ ID NO: 163:
SEQUENCE CRARACTERISTICS:
LENGTH: 9 amino acids
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OTHER INFORMATION: "XMP.332"
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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                                                                                                                         PRIOR APPLICATION DATA:
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US-07-907-190-13
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                                                               35.7%; Score 30; DB 2; Length 16; 25.0%; Pred. No. 1.4e+02; ive 6; Mismatches 3; Indels
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MEMORPHER READALF FORM:
MEMORPHER THE REPORT SHALLS
CONTRACT SHALL 
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STREET: 10 S. Wacker Drive Suite 3000
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 112-115-1100
TELECOMMUNICATION 112-124
INFORMATION FOR SEC 17 NO: 11:
SECURENC HARACTERISTICS:
LENGTH: 16 amino acids
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APPLICATION NOBER: US 07/915,923
FILLING DATE: 17-ULL-1992
ATTORNEY/AGENT INFORMATION:
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Patent No. 5523288
GRERAL INFORMATION:
APPLICANT: Chohen, Jonathan
APPLICANT: Kung, Adm H.C.
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ER: 26,949
                                                                       Query Match
Best Local Similarity 25.07
Matches 3; Conservative
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MOLECULE TYPE: peptide
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REGISTRATION NUMBER:
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Best Local Similarity
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US-08-311-611A-116
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PCT-US93-06552-11
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IIS-08-373-215-11
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10 S. Wacker Drive Suite 3000
                               MAME: ACCOMENT, OADE J
REGISTRATION WINDER: 36,99
REPRESENTED WINDER: 36,13-C
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TROUBLE CHARACTERISTICS:
LENGTH: 16 anion acids
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; Sequence 11, Application US/08373215
; Patent No. 5973110
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; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-485-937-11
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TOPOLOGY: not relevant
ATTORNEY / AGENT INPORMATION:
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STRANDEDNESS: not
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APPLICANT: Muller,
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                              MEDIUW TREE: FIODPY disk
COMPUTES: TRAFF COMPETABLE
OFERATION SYSTEM: CO.OS/ANS.OS
SOFWARE: PAREATIN RELEASE 81.0, VERSION 81.25
AURICATION FORMER: US/OS/AY2.783
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,105
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STATE: 111110018
STATE: 111110018
ZIP: 60606-6402
ZIP: 60606-6402
WEDJUW TYPE: Floppy disk
OGMUTER: Floppy disk
OGMUTER: TISH PC OGMUTER: 18100 PC
OGMUTER: 1810 
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PRIOR APPLICATION DAAN:
APPLICATION NUMBER: 08/273,540
FILING DAFIE: 11-10L-1994
FRIOR APPLICATION NUMBER: 08/209,762
FILING NOWE: 11-10R-1994
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Patent No. 5627153
GENERAL INFORMATION:
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**PELEVEN: 25.366

**TRIPEN: 25.366

**SEGURATION FOR SEGUR D. NO. 116:

**SEGURATION FOR SEGUR D. NO. 116:

**SEGURATION FOR SEGURATION SEG
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APPLICATION NUMBER: 08/273,540
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CTHER INFORMATION: "XMP.120"
US-08-372-783-116
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US-08-372-105-116
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    Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive

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6300 Sears Tower, 233 South Wacker Drive
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COMPUTER: IN PC COMPACINE.
SOFTWAKE: PC-TOSA/MS-TOS
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TELEX. 25-38/41-0448
INPORMATION FOR SED ID NO: 116:
SEQUENCE CHARACTERISTICS.
LENGTH 15 anno acids
TYPE: amino acids
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CTHER INFORMATION: "BPI.120"

US-08-311-611A-116
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TELEPHONE: 312/474-6300
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STATE: Illinois
COUNTRY: USA
ZIP: G0606-6402
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                                                                                                                                                                                                                      RESULT 13
US-08-372-783-116
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Query Match 34.5%; Score 29; DB 1; Length 15; Best Local Smilarity 62.5%; Pred. No. 1.9e+02; Matches 5; Conservative 1; Mismatches 2; Indels Matches 5; Conservative 1; Mismatches 2; Indels
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Job time : 36 secs
                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature

// OTHER INFORMATION: "BPI.120"

US-08-306-473a-116
                                            116:
                                    INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHRANCERSITICS:
LENGTH: 15 amino acid
TYDE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
       TELEFAX: 312-715-1234
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Pred. No. 1.9e+02,
1; Mismatches 2; Indels
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HEDINI TYPE: Floppy disk
COMPUTER: IN PK COMPUTER
OFFERTING SYSTER: FC-DOS/AS-DOS
SOFTWARE: Feterin The Steesee #1.0, Version #1.25
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretis Witcoff, Ltd.
STREET: Suite 3000, 10 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/306,473A
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10-206-473A-116

Sequence 116, Application US/08306473A

Patent No. 5567323

GURBAL INFORMATION:

APPLICANT. LITLE, ROGE 6.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.120"
US-08-372-105-116
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REPERENCE/DOCKER NUMBER: 93.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 62.5%;
Matches 5; Conservative
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amino acid
SY: linear
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STATE: Illinois
COUNTRY: USA
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29.7%; Pred. No. 1.2e+02;
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Pred. No. 25;
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Best Local Similarity 44.48;
Matches 8; Conservative
      22 VTFHVPSNVPLKEVLWKK 39
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                     January 28, 2003, 08:58:30 ; Search time 55 Seconds
                                     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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B81350
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S66035
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S12957
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Match Length DB
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Maximum DB seq length: 61
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Perfect score:
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Conser, 1-47-2000 Regulera_gravitor in the Troop Conser, 2-43-4-4002

Chartelland Regulera_gravitor in the Troop Conservation and Troop C
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A.Experimental source: serotype 02, strain NCTC 11168
C:Genetics:
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Procession, 00.0464

Proc. Not. And. Sch. 12, Meson Garcia, M.; Stoke, B.; Schlastager, D. H.; Schally, A.V. Proc. Not. And. Sch. 10.4, A. 23, MSC-26, 1885

Analysis and an anion orid sequence of the control original sector from pight Analysis and anion acid sequence of the control original sector from pight Analysis and anion orid sequence or School original sector from pight Analysis and School original sector from pight
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C.Comment: This protein is a transcription factor to act in the forespore chamber of the
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A Mendadone : 400 GHIDA MONDOLISH; GBARODOSIJ; NID.96458594; PIDN:AATIONBO.1; PID.964585]
A Experimental Source: strain Rl
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R. Chicassion (1994);
S. M. Sham, A. Haidalberg, J.F. Hickey, E.K. Peterson, J.D. Dodmon, R.J.;
S. M. Sham, V. Wonderey, J. Transco, C. M. Wooden, C. J. Statemari, C. J. M. Science, 286, 1571-1577, 1999.
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C.Species: Sus scroot admessing (domestro pig) 919.
C.Species: 30-Jun-1987 seaquence_revision 30-Jun-1987 *text_change ll-Apr-1997
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Pred. No. 4.4e+02;
1; Mismatches 4; Indels
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A; Reference number: JC6187; MUID: 97169156; PMID: 9016963
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A; Residues: 1-41 <PAT>
A; Note: 40-Ile was also found
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A: Residues: 1-55 <SHC>
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A;Start codon: TTG
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Ankanduse: 155 4500
Ankaptimental source: 881299104, GB:AL009126; NID:92632267; PIDN:CAB1791.1; PID:e11819
Ankaperimental source: 881299104
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C.Species: Bock-1995 Segenence_revision 13-Mar-1997 #text_change 15-Oct-1999
C.Accession: SeG035, B69736
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Bost Local Similarity 31.7%; Prod No. 6.2e402; 
Matches 13; Conservative 7; Mismatches 14; Indexs
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Job time : 57 secs
                                                                                                                                                                                 yaaB protein - Bacilius subtilis
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Nucleic, Ordan Res. 28, 431-4311, 2000
A. Reference Packer General Sequence of the statistical induction and
A. Accession: RESES A. R.S. Patrio 262:376; M.F.D. 118312
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A:Experimental source: strain C-125
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A.Experimental source: strain CML029
C;Genetics:
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Asketter General Z.; J. 385-389
A. Réference manuber; A. 72000; MOID: 992-06666; PMID: 1019-2988
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C:Species: Chimaydophila pneumoniae. Chimayda pneumonies (Cspecies: Chimaydophila pneumoniae. Chimayda pneumoniae.
C: Dates: 23-04-1399 * Sequence_revision 23-Apr-1599 * Next_change 05-May-2000
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B; Conservative 4; Mismatches 5: Indete
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A;Map position: circular chromosome
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A;Molecule type: DNA
A;Residues: 1-48 <STO>
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A:Molecule type: DNA
A:Residues: 1-51 <ARN>
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-43 <KUR>
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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(Rel. 12, Last sequence update)
(Rel. 40, Last annotation update)
II reaction center T protein.
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Antibiotic: Amphibian skin; Amidation.
MOD_RES 22 AMIDATION.
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36 LWKKQKDKVAEL 47
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Copyright (c) 1993 - 2003 Compugen Ltd.
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THPA_THADA
NU3M_NEUCR
RL33_RICCN
YOR7_TTV1
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CR32_LITCE
YAAB_BACSU
RK32_ODOSI
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IVBC_NAJNA
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PSBT_MAIZE
PSBT_TOBAC
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RL35_MYCFE
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Y260_BACHD
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RLX_HALMA
CR34_LITCE
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                         ... Chem. Res. 138:510-936(1993).
... Chem. Res. 178:510-936(1993).
... Chem. Res. THERACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL CONFONMATION HAITCH CAN DISRUPE BACTERIAL MEMBRANES. BACH CARRIN DISRUAYS A DIFFERENT ANTHATROBANG SPECIFICITY.
Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.; **Peptides from Australian frogs. The structures of the caerins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vistracture and function of the region of the replication origin of the Benilius subtilis (horacsome. III. Nucleotide sequence of some tide Benilius subtilis (horacsome. III. Nucleotide sequence of some Nucleic Acids Res. 13:2321-2255(1985).
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01-0CT-1994 (Rel. 30, Last sequence update)
11-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein yaaB.
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2 LWEKTKEKASEL 13
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                                                                                                            Litoria caerula.
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WORKTION: EXAFT FUNCTION NOT KNOWN, IT 18 ESERWITAL TO MAINTAIN PHOTOSYMPHETIC ACTIVITY UNDER ADVERSE GROWTH CONDITIONS
                                                                                                                                         Enkaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta; Sperantophyta; Magnollophyta; Liliopsida; Poales; Poacea; Enhartodese; Oryzas; Oryza; Ory
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Ampliba; Bartenia; Anura; Meobatrachia; Bufoncidea; Hylidee;
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Probom: POD04453: PSII_PBDr; 1.
Procosynchesis: Phocosyetem II; Chloroplast; Transmembrane;
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16-CCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Litoria caerulea (Green tree frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND MASS SPECTROMETRY.
TISSUE-Perotoid gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001743; PSII_PSbT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 AA; 4045 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.5%;
35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 GIIFPAIFFREPPKVPTKKV 34
                   Oryza sativa (Rice), and
Populus deltoides (Poplar).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 35.0 tes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR32_LITCE
P56239;
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CR32_LITCE
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This SMISS form entry is operjuith. It is produced through a collaboration between the Suiss institute of inclinionatius and the RBML collaboration between the Suiss institute. There are no restrictions on its inclinional institute. There are no restrictions on its modified and this statement is not removed. Uses the Suiss all comes agreement (see Note). Wew'ish with commercial entities requires allcomes agreement (see http://www.ish.wib.cib.ch/mnounce/or sends an easil to literatefab-tib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMARANESS / Fischer II. II. Hichalpowit C.B., Annarella M., 
Dorfelbard M., Silrecon II. II., Michalpowit C.B., Annarella M., 
Raigo Y.Y., Sallacher M. M., Chous E., Memana Spallart C., 
"The complete agentee of the cynnelle second of Chapteria paradoxa. 
The complete complexity of a pulsative paintid." (i) Signed M. C. M., Hermann M. A., Jose N. M., Membler N. E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nuclectide sequence of the cyanelle DNA from Cyanophora paradoxa."; Plant Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STREATH-LB555 / Pringshelm;
Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38.5; DB 1; Length 39;
Pred. No. 3,3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
                                                                                                                                                                                            Score 39; DB 1; Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15: Indels
                                                                                                                                                                                                                                                                                      3; Indels
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Photosynthesis; Photosystem II; Cyanelle.
SEQUENCE 39 AA; 4246 MW; FC42C8907BBE96B2 CRC64;
                                                                                                  5253B73505AFA3C0 CRC64;
                                                                                                                                                                                                                                         Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Photosystem II reaction center X protein.
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(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
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                                                              RY STMILARITY
                                                                                                                                                                                                                                                                                      5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
                                                     INIT_MET 0 0
SEQUENCE 57 AA; 6374 MW;
                                                                                                                                                                                            11.98;
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                                                                                                                                                                                                                                                                                                                                                                                33 KEVLWKKQKDKVAE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 RKSVWKKKADKAAK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (eqs.);
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P48266;
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16-0CT-2001
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P19859;
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A process E., Pajic D., Parrelle B., Rapport G., Noy W., Reynolds S., Ray W., Konthan C., Chockel E., Nose W., Sadai S., Ray W., Konthan C., Chockel E., Nose W., Sadai S., Songola M., Agnor C. C., Sadai S., Songola M., Saco C. S., Serror D., Shin B.S., Sada B., Songola M., Saco S., Sadai S., Sada B., Saco M., Saco S., Serror D., Shin B.S., Sada B., Songola M., Wondon M., Yogherte E., Songola M., Vanna C., Yang M., Wander E., Welder E., 
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"The Altroplass geneme of a chicoophyll at-recentaining alga.
Double in Balmemel 13:356-341(19595).
"- SIMILARITY: BELONES TO THE 1329 FAMILY OF RIBOSOMAL RECENTS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
NCBT TaxTD=2849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEGUENCE 52 AA: 5932 MW: 3C7BF6AD3B4D577F CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SOCIYGVYGNVTPHVPSNV-PLKEVLWKKOKDKVAELENS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 TRDIVGI-----FDFKANMSPIVEEFLKKQKHKVVPSVNA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.5; DB 1;
Pred. No. 3.3e+02;
7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 3). Created)
01-FEB-1996 (Rel. 3). Larg sequence update)
16-CCT-2001 (Rel. 40. Last mendration update)
16-CCT-2001 (Rel. 40. Last endoaction update)
16-CCT-2001 (Rel. 40. Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Odontella sinensis (Marine centric diatom).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002677; Ribosomal_L32p.
Pfam; PF01783; Ribosomal_L32p; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X02369; -; NOT_ANNOTATED_CDS.
EMBL, D26185; BAA05241.1; -;
EMBL, 299104; CAB11761.1; -;
Subtitlst; BG10069; yaaB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997).
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58.3%;
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                                                                                          36 LWKKQKDKVAEL 47
                                                                                                                            2 LWEKIKEKANEL 13
           Best Local Similarity
Matches 7; Conserv
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SPECIES-Maize:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lotus japonicus.
                                                                                                                                                                                                                                                                                         PSBT_MAIZE
P37257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chloroplast
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                                                                                                                                                                                                                                                                   PCRT MATZE
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                                                                                                                                                                                                                                                                                         Shafqet 7. Zadiğ EH. Joservall H.;
Tarlicacion and characterization of a chymotrypsin Kumitz inhibitor
Ptype of Polypeptide from the vence of cobra (Naja naja naja).";
FRESHE Lett. 2735:6-8(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL GLANDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps

    - FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPIA HELICAL
CONFORMATION WHICH CAN DISROPT BACTERIAL HEMBRANES. EACH CARRIN
DISPLAYS A DIFFERENT ANTIANCROBIAL, SPECIFICITY.

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Peptidas from Anstralian frogs. The structures of the ceerins from
Litoria caerula."; 2010-206(1993).
     Venom chymotrypsin inhibitor.
Naje naje (Indian cobra).
Rokaryota, Metazos: Chordata; Craniata: Vertebrata; Bureleostomi;
Lopidosauria: Squamata; Scleroglosas; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Litochia costules (Green tree frog).
Mokrayote; Metezcos (Dozdete, Creniste, Vertebrata, Buteleostomi;
Amphiblia, Batradhia, Annra; Neobatrachia; Bufonoides; Hylidae;
Pelodryadines, Litocia.
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4BFB26A010C1737A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARIY: CONTAINS 1 BPT1/KUNITZ INHIBITOR DOMAIN.
PIR, S12957; 812957.
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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BY SIMILARITY.
BY SIMILARITY.
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Antibiotic; Amphibian Skin; Amidation.
MOD-RES. 22 22 AMIDATION.
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Fram. PPODO14, WANTE, BFTT. 1.
PRINTS, PROFOSTS, MACETERAB.
PROFOSTS, MACETERAB.
PROFOSTS, WANTE, BFTT. 1.
PROFITE, PSOFOTS, BFTT, KNUTE, 1.
PROFITE, PSOFOTS, BFTT, KNUTE, 2.
WHOMEN SETIME PROFOSTS APPT. MANIET, 2.
PROFITE, PSOFOTS, BFTT, KNUTE, 2.
PROFOSTS, PSOFOTS, BFTT, KNUTE, 2.
PROFOSTS, PSOFOTS, BFTT, KNUTE, 2.
PROFOSTS, BFTT, KNUTE, 2.
PROFOSTS, BFTT, MANIET, BFTT, MANIET, BFTT, MANIET, 2.
PROFOSTS, BFTT, MANIET, BFTT, 
                                                                                                                                                                                                                                            TISSUE-Venom;
MEDLINE-91085579; PubMed-2262001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND MASS SPECTROMETRY.
TISSUE-Parotoid gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFGFISCFSQQIYGVVFGNVTF 24
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                                                                                                                            Elapidae, Elapinae, Naja.
NCBI_TaxID=35670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Matches 7; Conserv
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while stills story mark is openjulah. It is produced through a collisionstillo between the Suiss institute of Biolificametics and the BBBS obstation to Bangace and the BBBS obstation to Bangace institutes "from ear on restrictions on Its medit for and Districtions in the second to be a seco
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                                                                                                                 Gaps
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Rock C., Darkan A., Taylov R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIANG-53395841; PubMed-7666415.
Maior R. M., Meckermann K., 19101 G.L., Koessel H.:
Compiles sequence of the maize chloroplast genome: gene content,
hotspots of divergence and fine tuning of genetic information by
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-1. SUBCELLURARIY LOCATION: Chloroplast thylakoid membrane.

-1. SIMILARIY: BELOWES TO THE PERF PARILY.

-1. SIMILARIY: BELOWES TO THE PERF PARILY.
                                                                                                                 Indels
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Pred. No. 2.8e+02;
2: Mismatches 3
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02-CT-1994 (Rel. 30, Last Sequence update)
16-CCT-2010 (Rel. 40, Last annotation update)
16-CCT-2010 (Rel. 40, Last annotation update)
PSBT OR YCF8.
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EMBL; X86563; CAA60312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT:
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Pfam; PF01405; PSbT; 1.
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MaizebB; 85519; -.
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This SMISS PROT entry is oppright. It is produced through a collaboration between the skiss institute of sincindraties and the SME constitution the throughout micronamics institute. There are no restrictions on its act by more point, institutions along a last content of the c
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Pred. No. 6.2e+02;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                         Borrella burgdorferi (Lyme disease spirochete). 1928-3. Hatsamid Ip17 (Index 17 No (1p16), and Plasmid Ip28-3. PRIESTRIA SpiroChhetelase; Spirochetectose; Borrella.
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SROUENCE 49 AA: 5851 MW: E226B54320953273 CRC64;
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NCBI_TaxID-139;
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30-MAY-2000 (Rel. 39, Created)
MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
BEDOZ AND EDERGE PECCET BEDOZ/BER03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          051014;
0447-2000 (Rel. 39, Created)
30-MA-2000 (Rel. 39, Last sequence update)
1-c-r--2001 (Rel. 40, Last annotation update)
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MERIDDARIK K., Olimo K., TORAKA M., WAKABURI T., BRYARILDE M.,
MERIDDARISH T., "ALE M. COLUMNOSSE A.; OSCHOLE M.
MERIDDARISH T., "ALE M. COLUMNOSSE A.; OSCHOLE M.,
MERIDDARISH T., "ALE M. COLUMNOSSE A.; OSCHOLE M.,
TORAKO M., Silmode M., SOGHICH M.), "TORAKO M., "Silmode M., "Sollich M.,
THO COMPLETE M. SOGHICH M.), "SOGHICH M.), "TORAKO M., "TORAKO M.
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Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPRONI41; PSII_PSDT.
Prdm. PF01405; PSDT. 1.
PRODOS, PROM. PROFESS. PSII_PSDT, 1.
PROCOSPITHERS: PROFESSEE II; Chloroplast; Transmembrane; PNylakoid.
                                                                                                                                  Score 37; DB 1; Length 33;
Pred. No. 4.2e+02;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
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             33 AA; 3818 MW: A51F72A372756A79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-00T-1989 (Rel. 12, Created)
01-00T-1989 (Rel. 12, test sequence update)
16-00T-001 (Rel. 40, tast amoutation update)
16-00T-001 (Rel. 40, tast amoutation update)
PSBT OR YCP8.
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SO THE RESULT OF COORDINATE REPORT OF COORDINATE SERVICES OF COORDIN

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whis strice year entry is opergight. It is produced through a collaboration between the SAHS institute of Epoinformatics and the BBEC outstation. The Bancepan inforfaments institute where are one restrictions on its use by non-point, institutions as loops as its optical soft institutions as loops as its optical and institute and institute and institute and institute allocate agreement (see http://www.isb-sib.ch/dnnounce) send an equal to Licensedsis-sib.ch/dnnounce)
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-i- SUBGELLUIAR LOCATION: Nuclear, nucleolar.
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13-B-2UN-2002 (Rel. 41, Last amontation update)
PAP protein (Transactivating regulatory protein) (Fragment).
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WANTING-6211733; PARMED-812230;

OFILIDIA R. TANGIT Facility all ADMISSION Of the Sex-determining
THE FEATURE THAN ADMISSION OF THE SECURITY OF THE SECURI
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BMG_18_PRO505; BMG_20x.
SMART: SMO0198; BMG_1
SMART: SMO0198; BMG_1
SMART: SMO0198; BMG_1
SMART: SMO0198; BMG_1
SMART INTERPRETATION: Activator;
         Cotton M.D., Horst K., Roberts K., Hatch B.,
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Enkaryota; Metazaa, Iorindata, Crafata, Vertebrata Dieteleosromi;
Mommalia, Butheria, Primates; Catarinini, Cercopithecidae.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last sequence update)
Sex-determining region Y protein (festis-determining factor)
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6.2e+02;
7; Indels
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Pred. No. 6.2e+02;
                                                                                          Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                  -1 - SIMILARITY: STRONG, TO B.BURGDORFERI BBD02 AND BBH03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 49 AA: 5808 NW; E226B544F12F3273 CRC64;
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                                                                                                                                                                                     Nature 390:580-586(1997).
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         Smith H.O., Venter J.C
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NCBI TaxID-9541;
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

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January 28, 2003, 08:58:05 ; Search time 28 Seconds (Withbout alignments) 448:888 Million cell updates/sec

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327
1_HCPGFISCPSQQIYGVVYGDKVAELENSEFRAFSSFKNR 61 Perfect score: Scoring table: Sequence: Title:

671580 segs, 206047115 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

46985 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 61

Database :

sp_rodent:* sp_virus:* sp_vertebrate:* sp_unclassified:* sp_rvirus:* sp_bacteriap:* sp_archeap:* sp_phage:* sp_plant:*

Pred. No. 1s the number of results predicted by chance to have a zero greater than or equal to the sore of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	09qv70 rattus sp.	098239 tapirus bai	098240 tapirus ind	098241 diceros bic		098243 diceros bic	098244 ceratother1	098246 rhinoceros	008574 catharanthu	P82126 sus scrofa	G9gz92 plasmodium	09ua59 caenorhabdi	09qz98 plasmodium	09xjb5 streptococc	Q45682 bacillus su	Q95600 squalus aca	
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ALIGNMENTS.

RESULT 1

					(e)			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom	Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Rurinae; R					Dudley M.A., Hachey D.L., Quaroni A., Hutchens T.W., Nichols B.	J.1	"In vivo sucrase-isomaltase and lactase-phlorizin hydrolase tur			:64;
	AA.			update)	on updat			ertebrat	i; Murid					chens T.	Reeds P.	hlorizin			1D07 CRC
	19 AA.		(p	ednence	nnotatio	ent).		iata; V	rognath					A., Hute	ok G.,	ctaserp		3).	0A8155A
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	PRELIMINARY;		BLrel. 13,	BLrel. 13,	01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	Lactase-phlorizin hydrolase (Fragment).		ia; Chordat	a; Rodenti				MEDLINE=93293888; PubMed=8514793;	ey D.L., C	erkinson J	1somaltase	rat.";	J. Biol. Chem. 268:13609-13616(1993).	SEQUENCE 19 AA; 2174 MW; 136CC0A8155A1D07 CRC64;
	PRELI		OO (Trem	OO (Trem	HOO (Trem	hlorizin		; Metazo	Butheri	D-10118;			13293888;	A., Hach	ler J., P	sucrase-	ed adult	Chem. 26	19 AA;
20	050v70	090v70;	01-MAY-26	01-MAY-26	01-MAY-26	Lactase-p	Rattus sp.	Eukaryota	Mammalia;	NCBI_TaxID=10118;	[7]	SEQUENCE.	MEDLINE=5	Dudley M.	Rosenberg	"In vivo	in the fed adult rat.";	J. Biol.	SEQUENCE
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0; Gaps Score 47; DB 11; Length 19; Pred. No. 48; 5; Indels 5; Mismatches 5; Indels Query Match 14.4%; Best Local Similarity 44.4%; Matches 8; Conservative

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60 AA. PRT; 22 VTFHVPSNVPLKEVLWKK 39 1 VIDSLPSEVPRAKIVWER 18 PRELIMINARY: 098239 RESULT 2 098239 DATE PE Q ò

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Makaryota, Metkazoa, Chordata, Craniata; Vertebrata, Euteleostomi: Memmalla: Eutheria; Perissodactyla; Rhinocerotidae; Diceros.
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Mediaryota, Mefrala, Perissodactyla, Rhinocarotidas, Duteleostomi:
Manmalia, Butherla, Perissodactyla, Rhinocarotidas, Diceros.
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Pred, No. 3.1e+02;
8; Mismatches 8; Indels
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11)
Frace C. A. Ryder C. A. No. A.
Frace C. A. Ryder C. A. See C. See C.
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FRAME D.G. "MAGE C.A.; PETSSOCHETJA.".

FRAME D.G. "MOSTOPHER IN THE PETISSOCHETJA.".

SUBMILTED (DEC.1998) to the EMBL/GenBank/DDBJ detabases
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60 AA: 6870 MW: 053450D5313F4A91 CRC64;
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01-MAY-1999 (TrENBLrel. 10, Last sequence update)
01-DEC-2001 (TrENBLrel. 19. Last annotation update)
MHO člass II DR-alpha (Fragmant).
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01-MAY-1999 (TREMBLEA]. 10, Last sequence update)
01-DC-20(TREMBLEA]. 19, Last annotation update)
MHC Class II DR-alpha (Fragment).
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                                             Don.:
Tapitus bairdii (Baird's tapir).
Bekaryota, Metzaca, Chorddta, Craniata, Vertebrata; Buteleostomi;
Mommalis, Butheria, Perissodacryia; Tapiridae, Tapirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tapirus indicus (Asiatic tapir) (Malayan tapir).
Bukatyota: Metazoa; Chordata; Crandata; Werkebrata: Euteleostomi;
Mammalia; Eutheria; Perissodactyia; Tapiridae; Tapirus.
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La; Eutheria; Perissodactyla; Rhinocerotidae; Diceros
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.8%; Score 45; DB 7; Length 60; 30.0%; Pred. No. 3.18+02; Live 8; Mismatches 8; Indels
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Pred. No. 3.1e+02;
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Figures From H.A.

Talk Figure 0. A. the reisonderyla.".

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01-087-10-09 (TrEMBIACE). 10, Created)
01-087-1099 (TrEMBIACE). 10, Last sequence update)
01-08C-2000 (TrEMBIACE). 19, Last sequence update)
MHC Class II DR-slpha (Fragment).
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01-MAY-1999 (TrEMBLrel. 10. Last sequence update)
01-DEC-2001 (TrEMBLrel. 19. Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 GNVTFHVPSNVPLKEVLWKKOKDKVAELENSEFRAFSSFK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GDEIFHV--DMEKKETVWRLE------BFGRFASFE 41
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Enematophyta; Magnoliophya; endicotyledous; core endicots; 
Asteridae; euskeride; l'Gentlandles; Apocyaceee; Rauvolifoldeae; 
Noues, Caharanhus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, X69785; CANA9440.1; -. Oxidoreductase; Monooxygenase; Electron transport; Transmembrane;
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01-509-1996 (TremEnter) 01. Last sequence update)

01-509-200 (TremEnter) 11. Last amontation update)

92-controme - 14-50 (EC 1.14.14.1) (CR13) (Frangment).

95-60-11. For example 1.
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Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ho S.-C., Wakatsuki S., Arioka M., Yamasaki M., Kitamoto K.;
                                                                   Length 60;
                                                                                                                               8: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: INDOLE ALKALOID SYNTHESIS.
-!- SUBCELLUTAR LOCATION: MEMBRANE BOUND.
-: SIMILARIYY: MEMBRE OF THE CYTOCHROME P-450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 1 1 1
SEQUENCE 42 AA; 4641 MW; 23CB3C9ABA4B34B4 CRC64;
BP2150D52634269B CRC64;
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                                                                                                                                                                                                  20 GNVTPHVPSNVPLKEVLWKKQKDKVAELENSEFRAFSSFK 59
                                                                                                                                                                                                                                                                      14 GDEIFHY--DLEKKETVWRLE------EPGRFASPE 41
                                                                                              Pred. No. 3.1e+02;
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                                                                   Score 45; DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 MSPAIPNVTLPLAQLLLHPDWKSAVGKLEDLDMTEAR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       42 AA
                                                                                                                               8: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93283641; PubMed-8507838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.6%;
                                                                   13.8%;
60 AA: 6868 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY:
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PubMed-9538211;
                                                                   Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-G. DON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ
      SECUENCE
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P82126;
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                                                                                                                                                                                                                                                                                                                                                                          PRSITE 9
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                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ceratotharium simum (White rhimoceros) (Square-lipped rhimoceros).
Eukaryota: Wetazoa; Chordata: Cramista: Vertebrata; Euteleostomi;
Nammalia: Eutheria; Perissodactyla; Rhimocerotidae; Ceratotherium.
(NB_I_TaxID-9807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Perissodactyla; Rhinocerotidae; Rhinoceros.
NCBI_TaxiD-9809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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Pred. No. 3.1e+02;
                                                                                                                                                                                                  Match 13.8%; Score 45; DB 7; Length 60; Local Similarity 30.0%; Pred. No. 3.1e+02; ns 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signimer From N. N.

"Task Daynoplan in the perisodactyla.';
"Task Daynoplan in the testisodactyla.';

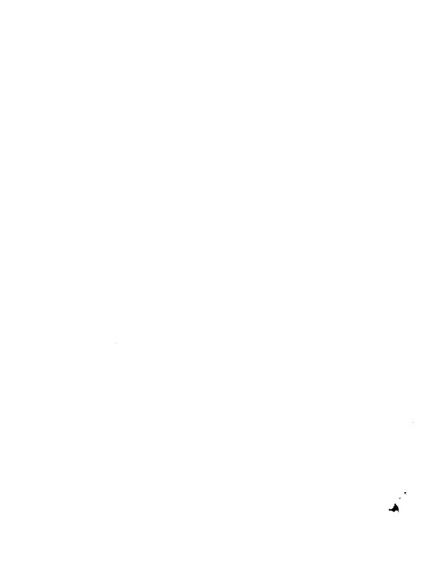
"Task Daynoplan in the perisodactyla.';

"Task Daynoplan in Task Daynop
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                                                                                                                                                                 60 AA; 6870 NW; 053450D5313F4A91 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MMC class 11 DR-alpha (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             053450D5313F4A91 CRC64;
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MAY-1999 (TERBLEC1 10, Last sequence update)
01-DEC-2001 (TERBLECE1 15, Last sequence update)
MRC Class II DR-alpha (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhinoceros unicornis (Greater Indian rhinoceros).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------EFGRFASFE 41
                                                                                                                                                                                                                                                                                                                                                                          20 GNVTFHVPSNVPLKEVLWKKQKDKVARLENSEPRAFSSPK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GDETPHY - DMEKKETVWRIE -----EPGREASPE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 GNVTFHVPSNVPLKEVLWKKOKDKVAELENSEFRAPSSFK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AA
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EMBL: AF113551; AAD19970.1; -.
InterPro; IPR001003; MHC_II_alpha.
Pfam: PF00993; MHC_II_alpha. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AA; 6870 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 GDEIPHY--DMEKKETVWRLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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SEQUENCE
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Matches
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                                                                                                                                                                                                                 "Genome sequence of the nematode C. elegans: a platform for fixmestlyshing biology, The C. elegans Sequencing Consortium."; States 282:2012-2018 (1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 5; Length 56;
Pred. No. 5.le+02;
Pred. No. 5.le+02;
Trdels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith A., Gibson A.;
The sequence of C. elegans cosmid W0485.";
Surbmatted (CT-1998) to the EMBL/GenBank-TOBM databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL: AF100305; AAC68914.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 IY-ITYGKVKNTDHELSNINGIKYYLRNVLPHEKNDKGOOYODLE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 IYGVVYGNV -- TEHVPSNVP-----LKEVLWKKQKDKVAELENSE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7834009C0C0293F7 CRC64;
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OSCISS
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01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
Hypotherical 5,6 KDs procein.
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Pred. No. 5.3e+02;
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                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 KKOKDKVAELENSEFRAFSSFK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 KRKOEEVNGEENSTWRSSSSF0 56
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33.3%;
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58 AA: 7148 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
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Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
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Q9GZ98
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                 2522555255525553525553
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- SOURCE, A LOCATION, INTEREST, ROBERONE SPECIAL SOLES WHERE IT I. SERVE SPECIAL SPEC
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"identification and characterization of porcine NP-190, a novel protein that is specifically expressed in the axonal membrane during the embryonic period." J. B. D. B. D. 23:132-138(1998).
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                                                                                                                                                                              -1- FUNCTION: IS A NEDROMAL ANTIGEN THAT MAY PLAY A ROLE IN BRAIN DEVELOPMENT. MAY BE INVOLVED IN NEURITE FORMATION OR AXONAL
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Plagmodium falciparum
Enkaryota Alvodata: Apicomplexa: Haemosporids: Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 6; Length 53;
Pred. No. 4.8e+02;
6: Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 5; Length 55;
Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 IYGVVYGNV--TFHVPSNVP-----LKEVLWKKQKDKVAELENSE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 AA; 6005 MW; D030BBE451B08D78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE8F57176E8797EF CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-007-2001 (TERMELRE). 18, Last sequence update)
01-007-2001 (TERMELRE). 19, Last annotation update)
NPPOCHELCAL 6.7 KDm protein.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                              GUIDANCE.
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NON_CONS
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Streptococcus thermophilus bacteriophage DT1.
Viruses disbak viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBL_TASTD=99410;
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Meuel C. Young M. Karamata D.
Genes concerned with blosynthesis of
Becliss subtilis are organised in two divergently transcribed
operons. ";
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Pupplessis M. Molnaud.
Tidentification of a genetic determinant responsible for host
Tidentification of a genetic determinant bacteriophages.";
Specificity in Streptococcus thermophilus bacteriophages.";
MOI. Wiscobiol. 41:325-336(2001).
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                                                                                                                                                                                                                                             STRAIN-011/15/7: pubmed-10049922;
Treeblab D. M. Molineau S., 'Complete genomic sequence of the lytic bacteriophage D71 of Straphococcus thermosphilus.";
Variology 255:63-76(1999).
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Pred. No. 4.9e+02;
6; Mismatches 11; Indels
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Pred. No. 4.6e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tremblay D.M., McIneau 8.;
Submitted (1406-1998) to the EMBL/GenBank/DDBJ databases.
EMBL. AR085222. AA021899.1.;
Fiypothet Cast protein.
SEQUENCE 48 AA. 5579 WM; 54988C06D27967B2 CRC64;
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Bal, MS797; AAA2846.1.
OBLWCE. 40 AA: 4769 MW; 03000EF83FE3FCCO CRC64;
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045662.366 (FIREMLIA. 01, Create, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 VVYGNVTFHVPSNVPLKEVLWKKQKDKVAELENSE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 IVNNNYTF---KRVP--KVLKPKVKELIADMVNDE 39
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Job time : 29 secs
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Local Similarity 37.1%;
es 13; Conservative
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Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CFGFISCFSQQI 14
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STRAIN-DT1;
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Q45682
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Human polypeptide
Human peptide #415
Human peptide #844
Peptide #441 encod
Peptide #874 encod
Protein #413 encod
Protein #413 encod
                                                                                                                                                                                                               Human brain express than both marked with the strong than the 
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human poptide enco
human ORP protein
eptide effecting
human ordionascul
BBL derived, pres
G-protein coupled
                                   Sheep erythrocyte
Sheep LFA-3 N-term
SEQ ID NO 454 from
   Sheep erythrocyte
Sheep erythrocyte
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18..23 /note- "linker"
24..38 /note- "pollen antigen"
                                                                    AAY19736
AAO08362
ABB27764
                                                                                                                         ABB28193
ABB32935
ABB3368
ABB18414
ABB18827
AAM54736
AAM54153
AAM66119
AAM66547
AAM66547
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AAM26396
AAM26833
AAM01731
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ABG35769
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AAB2461
AAR87199
AAR80764
AAR50765
AAR50765
AAR02956
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AAW02958
AAR50767
AAP82989
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   27-OCT-2000; 2000WO-US41646.
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Synthetic.
Cryptomeria japonica.
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AAB84103;
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Peptide
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AAB84103
Immune modulating
Immunomodulatory p
Immunomodulatory p
Immunomodulatory p
Immunomodulatory p
Sheep erythrocyte
Sheep erythrocyte
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Immunomcdulatory p
Immunomcdulatory p
                                                                                                                  January 28, 2003, 08:55:00; Search time 35 Seconds (without alignments) 232.237 Willion cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | $1102/jotabla.v/arenders/jonesserg/ neurol/1,043.00 pt/1;
| $1102/jotabla.v/arenders/ neurol/1,043.00 pt/1;
| $1102/jotabla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:*
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327
1 LHCFGFISCFSQQIXGVVFG......DKVAELENSEFRAFSSFKNR
              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                    fotal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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AAB84104
AAB84076
AAB84077
AAB84085
AAB84102
AAB84103
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Gapop 10.0 , Gapext 0.5
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Query
Match Length DB
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Maximum DB seq length: 61
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Perfect score:
Sequence:
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The specification describes an immensionalistory peptide construct.

Another measurement of the period comprises a first peptide sescotated with another more interesting to the period comprises a first peptide sessociated with another more interesting the period comprises a first peptide sessociated that another more comprises the period of cools and the manual responsion on a satisfact respectation of another manual response by the sec or makes of the couls to which the first period comprises the period of second peptide will be period to a stronger rate of the seriod of the couls to which will couns the second peptide will be period to a second peptide will be period to a second peptide will be a second peptide will be to a second peptide will be a second petide will be a second peptide will be a second petide will be a second be a second petide will b
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                                                                                                                                                                                                                            Novel immunomodulatory peptide construct useful for modulating an appropriate immune responses in an individual at risk for autoimmune dissease, allergic reactions, astrona or host-graft or graft-host disease
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asthma; host-versus-graft rejection; T cell; anergy; apoptosis.
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Pred. No. 0.00013;
1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 26; 55pp; English.
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/note- "linker"
24..35
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                                 (CELS-) CEL-SCI CORP.
                                                                                                                                                                WPI; 2001-374498/39.
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X L X B X R R X S X S X E L L L L L L X X X R X B
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The immunocolatory describes a fitter peptide associated with autonium of describes, allargy or station, or host-versus-specific rejection and which will hind to an antigen respect on a set of subset of realism and which will hind to an antigen respect on a set of subset of realism engages. The statement response to the statement of subset of realism the set of realism engages the statement of subset of realism the set of the statement of the second peptide will beind to peptide is attended. Alternatively, the second peptide will have the set on subset of realism to immunocolatory specified as our subset of realism to the second or subset of realism to whole of a subset of realism to whole of a subset of realism to whole set of subset of a tendamic allosses, altered; restcious a statem or a subset of realism to a tendamic and a second or subset of realism to a tendamic and a second or subset of realism to a tendamic and a second or subset of realism to a tendamic and a second or subset of realism to a tendamic and a second or subset of realism to a tendamic and a second or subset of realism to a tendamic and a subset of realism to a second or subset of the subset 
                                                                                                                                                                Novel immunomodulatory peptide construct useful for modulating an inappropriate immune response in an individual are risk for autoimmune disease, allerace immune cresponse in an individual are risk for autoimmune disease, allerace reactions, asthma or host-qraft or graft-host disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 VLWKKOKDKVARLENSEFRAPSSFK 59
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/note= "linker"
24..38
/note= "pollen an
                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 26; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200136448-A2.
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27-OCT-1999:

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Zimmerman DH;

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The specification describes an imminonalizery peptide construct.

The imminonalizery peptide constructs a first pertice associated with many and many the second lamme medicalizing spetide which will have a peptide as attached and manner and many 
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                                                                    Novel immunomodulatory peptide construct useful for modulating an inappropriate immune response in an individual at Tisk for autoimmune disease, allergic reactions, asthma or host-graft or graft-host disease
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100.0%; Pred. No. 0.00023;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                   Claim 3: Page 37; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VLWKKOKDKVAELENSE 17
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WPI: 2001-374498/39
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The immunochaltery peptide comprises a first peride associated with unformance disease, allergy of settlens, or poler-veters specific rejection unformance disease, allergy of settlens, or per-veters specific rejection unformance and the settlens of the settlens of the settlens of the first resettlens are specified as a specified as a stable of Tell to chief, the first container proposes of the one as a stable of Tell settlens of the one as a specified as a stable. As a stable of Tell settlens of the one as a stable of the second portion will cause the response to cause the settlens of the temperate of the other settlens of the temperate of another most operations. They are useful for readest of Tells in such containers reponse. They are useful for the temperate of another most period as a stable of the settlens of another most another the settlens of the settlens of the temperate of another most another the settlens and the settlens of the temperate of the settlens of the 
                                                                                                                                                                                                                                                                                                                                        Novel immunomodulatory peptide construct useful for modulating an inappropriate immune response in an individual ar risk for autoimmune disease, allergic reactions, asthms or host-graft or graft-host disease
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79.2%; Pred. No. 0.00022;
1ve 1; Mismatches 4; Indels
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                                             9905-0161734
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Matches 19: Conservative
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                                                                                                                  (CELS-) CEL-SCI CORP.
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Sequence Query Match

27-OCT-1999;

Zimmerman DH;

Unidentified.

AAB84077;

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Gaps

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The prediction describes an imminosolatory peptide construct. The prediction describes a minimisonalizatory peptide construct. The immunosolation of peptide comprises a first peptide sessociated with and which will hind to an antiper respect on a set in mass of all colds and minimison of the colds of th
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                                                                                                                                                                                                                                                                                                                                                                                                                               Novel immunomodulatory peptide construct useful for modulating an appropriate immune responses in an individual at risk for autolimune dissease, allergio reactions, astima or host-graft or graft-host disease
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asthms; host-versus-graft rejection; T cell; anergy; apoptosis.
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100.0%; Pred. No. 0.00054;
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24..42
/note= "pollen antigen"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 26; 55pp; English.
                                                                                             27-OCT-2000; 2000WO-US41646.
                                                                                                                                                                99US-0161734
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Cryptomerla japonica.
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                                                                                                                                                                27-0cT-1999:
                                                                                                                                                                                                                                                                                                      Zimmerman DH;
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18.23
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      27-0CT-2000; 2000MO-US41646.
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100.0%; Pred. No. 0.0029;
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24..42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.6%; Score 87; DB 22; L
100.0%; Pred. No. 0.00065;
ive 0; Mismatches 0;
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18..23
/note= "linker"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 27; 55pp; English.
                                                                                                                                                                       27-OCT-2000: 2000WO-IIS41646
                                                                                                                                                                                                                                    99US-0161734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 VLWKKOKDKVARLENSE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VLWKKOKDKVAELENSE 17
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nes 17; Conservative
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                                                                                                                                                                                                                                                                                                       CRES-1 CRE-SCT CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-374498/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 AA;
                                 WO200136448-A2
                                                                                                                                                                                                                                    27-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                   Zimmerman DH;
                                                                                                    25-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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1115 potents is used for immunished an animal and antibodosa are
stolated from the sears. These animals and animal and antibodosa are
stich haman 1115 glycoprotein in an immunosasy. Both the sheep and
human detred specificas are useful a immunosabulators.
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immunomodulators and for monoclonal antibody prodn.
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                                                Length 29;
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                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sheep erythrocyte target structure for T lymphocytes #3.
                                                                                                                                                                                                                                                                                                                                                    Sheep erythrocyte target structure for T lymphocytes #5.
                                                                                                                                                                                                                                                                                                                                                                                    erythrocyte target structure for T lymphocytes; (TllTS);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meuer S;
                                                Score 73; DB 9;
Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.049;
                                                                                   7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huniq T. Tiefenthaler G, Mitnacht R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 PSQQIYGVVYGNVTPHVPSNVPLKEVLWK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
                                                                                                                                                     59
                                                                                                                      11 SOOTYGVYYGNVTEHVPSNVPLKEVLWK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FSSDIYGAMGSVTFYVSESOPFTEIMLK
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                                                                                                                                                         2 SODIYGAMNGSVTFYVSESOPFTEIMFK
                                                                                                                                                                                                                                                AAP82989 standard; protein; 29 AA
                                                                                                                                                                                                                                                                                                                                                                                                     immune disease; immunomodulator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 9; 9pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.7%;
                                                46.4%;
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                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sest Local Similarity
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                 29 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP268995-A.
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                 Sequence
                                                                                                                                                                                                                                                                               AAP82989;
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                                                    Query Match
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                                                                                      Matches
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                                                                                                                                                                                                                                                             specific aceaple of Vertrainial segence of sheep virilis. The entire TIITS The entire TIITS protein is used for immufsing an enimal and matibodies are isolated from the senter. These afterfolders are in turn used to react with haman TIITS slycoprotein in an immunosasy. Both the sheep and haman destred proteins are useful as a immunosablators.

See 110 AARR0208, AARR02386, PARS988 and AARR02389.
                                                                                                                                                                      ......sericous sueep TIITS and human TIITS glycoprotein - useful as immunomodulators and for monoclonal antibody prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roungeneous sheep filts and human filtS glycoprotein - useful immunomodulators and for monoclonal antibody produ.
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheep erythrocyte target structure for T lymphocytes #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erythrocyte target structure for T lymphocytes; (TllTS);
                                                                                                        Meuer S:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 76; DB 9;
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hunig T, Tiefenthaler G, Mitnacht R,
                                                                                                        Mitnacht R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 PSOCIYGVVYGNVTFHVPSNVPLKEVLWK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FSQDIYGAMNGSVIFYVSESQPFTEIMGK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP82986 standard; protein; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immune disease; immunomodulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                          23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 9; 9pp; German.
                                                                                                                                                                                                                                  Claim 1; Page 9; 9pp; German.
   87EP-0008695
                                      86DE-3639920
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                                                                                                        Tiefenthaler G.
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                                                                                                                                           WPI: 1988-148827/22.
                                                                     (FARH ) HOECHST AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           29 AA
   19-NOV-1987;
                                  22-NOV-1986:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP268995-A.
                                                                                                        Hunig T.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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protects is used for jemenising a natial and artificidities are 
isolated from the secure. These artificidities are in intri used to reset 
with human THIRS spycoprotect in an immunosassy, Both the sheep and 
human destred proteins are useful as immunosablostors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mature form: human; ovine; LFA-3; antiviral agent; virus; infection propagation cycle; HIV; PCR; primer; sheep;homologue; D1D2 protein.
                                                                          Homogeneous sheep T11TS and human T11TS glycoprotein - useful as
immunomodulators and for monoclonal antibody prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An antiviral agent containing LFA-3 - useful on a virus with the
                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                     Score 62; DB 9; Length 29;
Pred. No. 0.71;
5; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Unidentified aming acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Unidentified amino acid"
             Meuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             same infection propagation cycle as HIV.
             Mitnacht R.
                                                                                                                                                                                                                                                                                                                                                                                                         11 SQQIYGVVYGNVTFHVPSNVPLKEVLWK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SXDIYGAMNGXVTFYVSESOPFTEIMXK 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 14; 18pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR60315 standard; Protein; 29 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sheep LFA-3 N-terminal peptide.
                                                                                                                        Claim 1; Page 9; 9pp; German.
                                                                                                                                                                                                                                                                                                                                        19.0%;
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             Tiefenthaler G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-1995 (first entry)
                                                                                                                                                                                                                                                                          See also AAP82986-P82989.
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                                             WPI; 1988-148827/22.
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                       29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                           Sequence
             Hunig T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR60315:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Specific example of W-translal sequence of sleeps IIITS. The entire TITS special is used for immunishing an animal and antibodies are its sociated from the serum. Prese antibodies are in turn used to react with human TITS diveptorietin in an immunosersy. Both the sheep and human detroit of the serum is a management of the special see a section is a managementation:
                                                                                                                                                                                                                                                                                                                    Momogeneous sheep TllTS and human TllTS glycoprotein - useful as
Ammunomodulators and for monoclonal antibody prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 64; DB 9; Length 29;
llarity 42.9%; Pred. No. 0.39;
Conservative 6; Mismatches 10; Indels
         erythrocyte target structure for T lymphocytes; (TllTS);
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                          immunomodulator
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Lafleur DR, Moore PA, N1 J, Olsen HS, Rosen
Shi Y, Soppet DR, Wei Y, Young P;
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.	OM protein - protein search, using sw model	Run on: January 28, 2003, 09:00:21; Search time 11 Seconds (11.15but alignents) plates/sec 11.169 Million cell updates/sec	Title: 16-09-730-465-2_COPP_20_80 Perfect score: 377 The Perfect score: 377 The Perfect score: 377 The Perfect score: 377 The Perfect Score Scor	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 122226 seqs, 20178551 residues	Total number of hits satisfying chosen parameters: 61208	Minimum DB seq length: 0 Maximum DB seq length: 61	Post-processing: Minimum Match On Asximum Settch 1004 Listing first 45 summaries	Database : Published_Applications_AA:*	11 A 1991 - 5, 4 (200 - 40 to 1, 4 (200 - 40 to 1) 4 (200 - 40 to	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	56 10 US-09-864-761-33712 56 10 US-09-864-761-34125	48 14.7 57 10 US-U9-764-869-1235 47 14.4 51 10 US-U9-799-514-19 46 14.1 59 10 US-U9-864-761-39695	43.5 13.3 33 10 0S-09-864-761-34725 43.5 13.3 46 10 0S-09-764-869-641	43.5 13.3 57 10 43 13.1 34 10 42.5 13.0 49 9	42 12.8 34 10 US-09-864-761-33625 42 12.8 34 10 US-09-864-761-34165 5 12.8 34 10 US-09-864-761-34165	12.6 53 10 US-09-0864-01.30220 12.7 58 10 US-09-0864-761-49002 12.5 28 10 US-09-864-761-46128	18 41 12,5 51 10 US-U9-864-761-34679 Sequence 24679, A 19 40.5 12.4 41 10 US-U9-997-498-2 Sequence 2, Appli

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LOCATION: (28)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION EXPRESSED IN PERFORMAL STORMA, 4
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OTHER INFORMATION EXPRESSED IN MOUTE TURB, STORMAL 3.2.3.
OTHER INFORMATION EXPRESSED IN MOUTE ALTER, STORMAL 3.2.3.
OTHER INFORMATION EXPRESSED IN MINE, STORMA, 3.2.3.
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NUMBER OF SED ID MOS: 2442
SOFTMARE: Patentin ver. 2.0
SED ID NO 1235
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Partern No 12002005051211
GREENL INFORMATION
APPLICANT: Rosen et ATTION
TITLE OF INVENTION, Sucleic Acids, Proteins, and Antibodies
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SEQ ID NO 34125
            PRIOR PARTICULOR SWINGER TOTAL TOTAL STATE STATE
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CURRENT FILING DATE: 2001-01-17
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Matches 13: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ISCFSQOIY --- GVVYGNVTFHVPSNVPLKEVL#KKOKDKVAELENSEFRAFSS 57
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PRIOR PAILOTRON NUMBER: PCF/ASOJ/OG670
PRIOR FILLING DATE: 2001-01-150
PRIOR PAILOTRON NUMBER: US 60/234,687
PRIOR PAILOTRON NUMBER: US 60/604.408
PRIOR PAILOTRON NUMBER: US 60/604.408
PRIOR FILLING DATE: 2000-06-10
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PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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Patent No. USZ002004875A1
PATENTAL INFORMATION
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APPLICANT Penn. Sharron 6.
APPLICANT Penn. Sharron 6.
APPLICANT: Can. Wenshing
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OTHER INFORMATION: MAP TO AP000087.1
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TITLE OF INVESTION: COMMONENTINGS AND PRINCIPAGE FOR THE DETECTION, DIAGNOSIS AND THER PITLE OF INVESTION: COLLOCAL MALICHANCIES.
FILE REPRESENCE, 2077-10.01.200 cc.10.21.00 cc.10.21.00 cc.10.21.00 cc.10.21.00 cc.10.21.00 cc.10.21.00 cc.10.21.00 cc.10.20.10.21.00 cc.10.21.00 cc.10.
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SEQ ID NO 33626
LEWITH: 35
                                                                                               PRIOR PLICATION NORMERS PETABOLOGIS PRIOR 
                                         APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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Publication No. US20020198362Al
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/200, 303
PRIOR ETLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200, 779
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
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46.7%; Pred. No. 47;
tive 4; Mismatches 4; Indels
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SEQ ID NO 34165
LENGTH: 34
PRIOR PATICATION NAMES (PLY/SSI)/70066
PRIOR FLIAND DATE: 2002-01-30 (PRIOR PLIAND PATICATION NAMES (PRIOR PATICATION NAMES (P
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PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763A1
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Matches 7; Conservative
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ORGANISM: Homo sapiens
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US-09-864-761-33626
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APPLICANT: Nems, SHATTON G.
APPLICANT: NEMS, DAVIG S.
APPLICANT: NEMS, DAVIG S.
TITLE OF INVESTION: GENER EXPRESSION ABALESTS BY MICHER ACID PROMESS USEFUL PO-
TITLE OF INVESTION: GENER EXPRESSION ABALESTS BY MICHERARMA CAPITAL SPECIAL STATES OF THE REPRESSIONS: A PARTICIPATION OF THE SPECIAL STATES OF THE SPECIAL SPECIAL STATES OF THE SPECIAL STATES OF THE SPECIAL SPECIAL STATES OF THE SPECIAL STATES OF THE SPECIAL SPECIAL STATES OF THE SPECIAL STATES OF THE SPECIAL SPECIAL STATES OF THE SPECIAL 
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OTHER INFORMATIONS INVESTEED IN LINES, SIGNAL = 6.4

OTHER INFORMATIONS INVESTEED IN BEACH, SIGNAL, 26.1 = 6

OTHER INFORMATIONS INTERESTEED IN BEACH, SIGNAL, 26.1 = 6

OTHER INFORMATIONS INTERESTEED IN BEACH, SIGNAL, 26.1 = 6

OTHER INFORMATIONS INTERESTEED IN BEACH, SIGNAL, 2.5

OTHER INFORMATIONS INTERESTEED IN BEACH, SIGNAL, 2.5

OTHER INFORMATIONS INTERESTEED IN BEACH, SIGNAL, 2.5

OTHER INFORMATIONS INTERESTEED IN AUGUST LITERS, SIGNAL, 2.5
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SQ ID NO 39655
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CURRENT APPLICATION NUMBER: US/09/864,761
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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PRIOR FILING DATE: 2000-05-26
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PRIOR FILLIN DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILLING DATE: 2000-10-04
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APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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: Sequence 34725, Application US/09864761
; Patent No. US20020048763A1
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THIE OF INVENTION: Inmunoglobulin Superfamily Polynucleotides, Polypeptides, and Ar
FILE REPERSMOE: PVIJSPI.
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THIAL OF INTENTION: HUBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION AMALYSIS BY MICHORARRA
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       ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-869-1235
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                                                                                                                                                                                                              22:
                                                                                                                               Query Match 14.7%; Score 48; DB 10; Length 57; Best Local Similarity 30.6%; Pred. No. 15; Watches 15; Conservative 6; Mismatches 6; Indels
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Best Local Similarity 28.6%; Pred. No. 18;
Matches 8; Conservative 7; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                     3 CFGFISC-----FSOOIY-----GVVYGNVT-FHVPSN 29
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PRICE PLING DATE, 2000-08-03
PRICE PLING DATE, 2000-09-03
PRICE PLING DATE, 2000-10-04
PRICE PLING DATE, 2000-10-04
PRICE PLING DATE, 2000-09-27
PRICE PLING DATE, 2000-09-27
PRICE PLING DATE, 2000-09-27
PRICE PLING DATE, 2000-09-37
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CURREMF FILMG DAFF: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/US00/23662
PRIOR PELICK DATE: 2000-08-29
PRIOR PELICK DATE: 109-09-09-09
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CURRENT FILING DATE: 2010-105-23
BRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APLICATION NUMBER: US 60/207,456
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763A1
GENERAL INFORMATION:
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Patent No. US20020065220A1
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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LENGTH: 51
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE ERRESSION ANALYSIS BY MICROARRAY
FILE REPERBACE: AGENICA-X-1
. NAMENTAL SITE
. LOCATION: (37)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-maino acids
18-09-74-689-641
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                     Query Watch 13.3%; Score 43.5; DB 10; Length 46; Best Local Similarity 38.5%; Pred. No. 44; WRtches 10; Conservative 3; Mismatches 10; Indels
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
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Weight Sept. 13722 Application US/09064761

Feature No. 120200004487534

GENERAL INFORMATION G.

APPLICANT: Rent, Sharton G.

APPLICANT: Hental Lavid R.

APPLICANT: Gen. (Newsheng
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CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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| OFFIRE NEOPANTON: TOPRESENDED HEART; SIGNAL = 18
| OFFIRE NEOPANTON: DEPRESENDED HEART; SIGNAL = 20.25
| OFFIRE NEOPANTON: DEPRESENDED HEART; SIGNAL = 20.25
| OFFIRE NEOPANTON: DEPRESENDED HEART; SIGNAL = 20.25
| OFFIRE NEOPANTON: DEPRESENDED HEART; SIGNAL = 3.45
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| OFFIRE NEOPANTON: DEPRESENDED HEARTON: DEPART SIGNAL = 3.45
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NUMBER OF SEQ ID MOS: 2442
SOFTHARR: Petentin Ver. 2.0
SEQ ID NO 641
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TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
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13.3%; Score 43.5; E
Best Local Similarity 26.5%; Pred. No. 29;
Matches 9; Conservative 10; Mismatches
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                          FECOR PATTACTON MANAGES FOR TOTATOS/OGGY PRODE FLIAMED TANES. 2001-01-30 PRODE FLIAMED TANES. 2001-01-30 PRODE FLIAMED TANES. PATTACTACTON MANAGES FOR TOTATOS/OGGES PRODE FLIAMED MANAGES. FOR TOTATOS/OGGES PRODE FLIAMED TANES. 2001-01-30 FOR TOTATOS/OGGES PRODE FLIAMED TANES.
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/00663
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Patent No. US20020061521A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-01-17
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT,
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Page 5

US-10-001-855-147 Sequence 147, Application US/10001835 Sequence 147, Application US/10001835 SPECIAL SECOND SECON	FRIOR PRILICATION ROBERS 66/143-997 FRIOR PLILING WHEE 5,000-11-30 FRIOR PLILING WHEE 2,000-11-30 FRIOR THE STATE OF	Oury Mark Lead Similarity 71.5% pred, 50, 51, 50 % Length 49, Marches 131, Conservative 9, Haraches 13; Index 27, 50 pps 2; Or 10 PROPERTY PROPERTY CHARACHER 13; Index 15 7; Gaps 27, 50 pps 27, 50 p		THILD OF THEMEN WHINDSON WHINDSON WHINDSON SHOULD FOON WICKLE OLD PROBES USEFUL PO- TILLE OF INVESTICATION CHORM PROPERSION MAINTERS BY MITOPOREMY THE REFERENCE. ACCOUNTS. 1. SERVICE STORM MAINTERS BY MITOPOREMY CHORMER APPLIANCE THOU MADER: USEFUL FOR THE ACCOUNTS. 1. SERVICE STORM PROPERTY ON MADER: USEFUL FOR THE ACCOUNTS. 2000-02-04 (0.740-2.11). FROM PRILING THE 2000-02-04 (0.740-2.11).	### PRINCE TO THE WINDOWS OF SEASON	PRIOR FLICATION DATE, 2001-01-30 PRIOR PRELICATION NUMBER: PST/9001/00669 PRIOR TAIL THOU NATE, 3001-01-30 (1906) PRIOR PRICE THING THE 2001-01-30 (1906) PRIOR PRICE THING THE 2001-01-30 (1906) PRIOR PRILICATION NUMBER: PST/9001/00669 PRIOR PRILICATION NUMBER: PST/9001/00669 PRIOR PRILICATION NUMBER: PST/9001/00663 PRIOR PRILICATION NUMBER: PST/9001/00663 PRIOR PRILICATION NUMBER: PST/9001/00662
PURESSED IN HEARY, SIGNAL = 1. PURESSED IN HEARY, SIGNAL = 1. PURESSED IN HEARY, SIGNAL = 1. PURESSED IN HEARY SIGNAL = 1. PUR	Our Melchinetty 15.4% Section 45.5; DB 10; Langth 57; Michael 21, Conservative 7, Missiaches 8; Indels 7; Caps 2; Michael 21, Conservative 10, Missiaches 8; Indels 7; Caps 2; Oy 19 YOMTSWY-YSWEATVARGORYALISES 50 Dp 17 YCMISGHWODPSNSHAWWARGORSA 45	URE ON 45 to 2.0.097) Programme of 0073 pepticetion US/0881242 Regions of US/2000001558An US/0881242 Regions Table of US/200001558An US/20000154 Regions Deadlerk, spect APPLICATE Obline, Rest L. APPLICATE Obline, ARCH L.	APPLICANT Tracted, John D. APPLICANT Cart. John D. APPLICANT Cart. Grant J. APPLICANT Namacio. Sebert I. APPLICANT NAMACIO. SEBERT NAMACIO. SEBERT NAMACIO. SEBERT NAMACIO. SEBERT NAMACIO. SEBERT NAMACION. SEBERT NAMACIO. SEBERT NAMACION. SE	RECOR APPLICATION BRIDGES 607-01-01 RECORD APPLICATION BRIDGES 607-00-646 RECORD APPLICATION BRIDGES 607-00-646 RECORD APPLICATION BRIDGES 607-00-70-70 RECORD APPLICATION BRIDGES 607-00-70-70-70 RECORD APPLICATION BRIDGES 607-00-70-70-70-70-70-70-70-70-70-70-70-7	PROBACTOR TO THE CONTROL OF THE CONT	Owery Metch Similarity 13.1%; Score 43; DB 10; Length 34; Set Catches 13: 10.1%; Score 43; DB 10; Length 34; Michies 9; Conseretive 9; Minmaches 11; Indels 0; Caps 0; N 13: NEVARKOGONYANESPRAKSERS 61 1 1: 11

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10 THER INFORMATION: EXPRESSED IN BRAIL, SIGNAL, = 2.2

10 THER INFORMATION: EXPRESSED IN BRAIL, SIGNAL, = 2.2

11 OTHER INFORMATION: EXPRESSED IN BRAIL, SIGNAL, = 2.2

12 OTHER INFORMATION: EXPRESSED IN WILLION: SIGNAL, = 1.3

13 OTHER INFORMATION: EXPRESSED IN WILLION: SIGNAL, = 1.3

14 OTHER INFORMATION: EXPRESSED IN FIRST, LIVER SIGNAL, = 1.3

16 OTHER INFORMATION: EXPRESSED IN FIRST, LIVER SIGNAL, = 1.3

16 OTHER INFORMATION: EXPRESSED IN FIRST, LIVER SIGNAL, = 1.3
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Pred. No. 47;
4; Mismatches 4; Indels
PRIOR PELCHYCON WHERE PETVASOL/JOGGI PRIOR PLANCE AND COL-19 (1-19) PRIOR 
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Patent No. US20020048763A1
GENERAL INFORMATION:
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Best Local Similarity 46.78
Matches 7; Conservative
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OTHER INTERPENTORS: EXPRESSED IN BRAIN, SIGNAL. # 1.3
OTHER INTERPENTORS: EXPRESSED IN BROWE WARROW, SIGNAL. # 1.3
OTHER INTERPENTORS: EXPRESSED IN ADULT LIVER, SIGNAL. # 1.3
OTHER INTERPENTORS: EXT_HURAN HIT: BE7.8655.1, EVALUE 3.60e+00
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PRIOR PARTICIPATION MORBERS PET/USD1/00661
PRIOR PLIAND DARKE, 2001-01-30
PRIOR PRIOR DARKE, 2001-01-30
PRIOR DARKE, 2011-01-30

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PRIOR APPLICATION WAMBER: PCT/US01/00665
PRIOR ELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PALOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763Al
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US-09-864-761-33625
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Search completed: January 28, 2003, 09:01:40 Job time : 15 secs

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57.1%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                               Score 46; DB 5; Length 44;
Pred. No. 33;
4; Mismatches 2; Indels
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COURSER APPLICATION MARK PROPERTIES PROPERTIES
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STREET: 419 Seventh Street, N.W., Suite 300
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPH*=2 PCT
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                         14.18;
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Best Local Similarity 57.18
Matches 8; Conservative
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INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
          LENGTH: 44 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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MOLECULE TYPE: peptide
                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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Best Local Similarity
                                                                                                                                                                  TOPOLOGY: linear
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PCT-US93-08528-306
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TITLE OF INVENTION: POLYPETIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
CORRESPONDENCES: 348
CORRESPONDENCE ADDRESS:
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Pred. No. 33;
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COMPUTER READMAIL FOODS:

WREITING TYPE: Floopy disk
COMPUTER: INN FOODS disk
COMPUTER: INN FOODS disk
SOFTHAM SYSTEM: FC-TOS/MS-TOS
SOFTHAMS: PAPELACINE TO Release #1.0, Version #1.25
APPLICATION UNDARA:
RAPLACINICATION DATA:
REPLICATION UNDARA:
RELEASE TOS DISK DISK DISK DATA:
RELEASE DATE:
RE
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
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REGISFRATION NUMBER: 34.740918
REFERENCE/DOCKEY NUMBER: MURPH=2 PCT
FELECOMMUNICATION INFORMATION:
TELEBRIONE: 202-628-5197
TELEBRIONE: 202-628-528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-32-8
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FILING DATE: 09-SEP-1993
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GENERAL INFORMATION:
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FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DRAM.
PRILING DATE: 10-SEP-1992
PATTORNEY/AGET INFORMATION:
NAME: TOWNSEND, KEVIN G. (933
REGISTRATION NUMBER: 34,033
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COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 305:
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INPORMATION POR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
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Best Local Similarity 57.1%
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US-08-118-270-306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.C.
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APPLICANT: SULPBY, SARGALI B.
TITLE OF INVERTION: POLIPPETTIES OF G-COUPLED PROTEIN
TITLE OF INVERTION: PRESERVORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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18 de 1147-07-016

19 de 1147-07-016

10 de 1147-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM YPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-1005/MS-005
SOFFWARE: Patentin Release #1.0, Version #1.25
SUFFWARE: APLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDT AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
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FILING DATE: 09-SEP-1993
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGGNT INFORMATION:
                                                                                                                                                                               Sequence 305, Application US/08118270
Patent No. 5508884
GENERAL INFORMATION:
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MUR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
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MOLECULE TYPE: peptide
US-08-118-270-305
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VYGLVDGLVTFYLP 17
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ZIP: 200
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                                                                                                            PESULT 11
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                                                                                                                                                                                                                                                                                                             Score 48; DB 2; Length 24;
Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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FILING DATE: 24-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/103,170
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OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 27, Application US/08103170
; Patent No. 5885824
                                                                                                                                                                                                                                                                                                                     14.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGNENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: DOG
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 53.39
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 24 amino acids
TYPE: amino acid
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 GIYGVVYGNVTFHVP 27
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MEDIUM TYPE: Floppy
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STATE: Virginia
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II SQQIYGVVYGNVTFHVPSNVPLKEVLWK 38

Sequence 3, Application US/08328152A Patent No. 5556943

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Gaps
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P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.5%; Score 54; DB 6; Length 11; Best Local Similarity 100.0%; Pred. No. 0.6;
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PREMENT, 8
PREMENT, 9
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APPLICATION NUMBER: 08 07/633,060
FILING DATE: 24-DEC-1990
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/07/237,309
FILING DATE: 26-AUG-1988
            2 SXDIYGAMNGXVTFYVSESOPFTEIMXK 29
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; Patent No. 5885824
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RECISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 236
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TELEPHONE: (703)521-4500
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INFORMATION FOR SEQ ID NO:
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COUNTRY: U.S.A.
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                                                   APPLICANT: Obtasalta, seo]
APPLICANT: Obtas. Takeaki
APPLICANT: Obtas. Takeaki
APPLICANT: Obtas. Takeaki
APPLICANT: Obtas. Seo.
APPLICANT
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MEDIUM TYPE: FORDER VALUE
OMERTER: INM FC COMPUTER:
OMERTER: FC COMPUTER:
FC COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: ANGETONG, WESTERMAN, HATTORI MCLELAND
ADDRESSEE: MAGGHTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1725 K Street N.W., Suite 1000
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FILING DATE: October 24, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: District of Columbia
COUNTRY: United States of America
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REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 920366A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-JUL-191
PRIOR APPLICATION NUMBER: JP JP151377
APPLICATION NUMBER: JP JP173764
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP JP151792
FILING DATE: 24-JUN-1991
PRIOR APPLICATION DATE:
APPLICATION NUMBER: JP JP154486
FILING DATE: 26-JUN-1991
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APPLICATION NUMBER: JP JP134789
PILICH DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP JP151792
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SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
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(202) 887-0357
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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US-08-328-152A-3
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GENERAL INFORMATION:
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LENGTH: 24 amino acids

TYPE: amino acid

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Gaps
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TITLE OF INVESTIGATION IN THE SEQUENCES, RECOGNISMAT DAY
MOLECULES AND PROCESSES FOR PRODUCING PI-LINNED LYMPHOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 FSQQIYCVVYGNYTFHVPSNYPLKEVLWKKQKDKVAEL 47
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FILING DATE: 26-AUG-1988
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                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
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INFORMATION FOR SEG ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 50 amino acids
875 Third Avenue
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES: 41
CURRENT APPLICATION DATA:
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                                                                                                                       New York
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;Patent No. 5185441
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US-08-328-152A-3
                                                                                                            STATE: N
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                                                                                                 APPLICAME: 1050A, MASTGARET D.
17TLE OF INVENTION: CO2-38NOIRO DOBALN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
TOWNERS OF SUCCESSES 3
COURSESSES 15
COMPENSES: 151AA (NAVOR
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FILTING DARK MACE 1934 2000
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FILTING DARK 1934 1937 1937
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APPLICATION NUMBER: US 07/940,861
FILING DATE: 21-OCT-1992
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
PCT-USS2-02050-2
PCT-USS2-02050-5
PCT-USS
WALLNER, Barbara P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212)715-0673
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LENGTH: 50 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOGEN, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç
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1 PSQQIYGVVYGNVTPHVPSNVPLKEVLWKKQKOKVAELENSEFRAFSSFK 50
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                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-459-657-2
                                                                                                         US-08-459-657-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP:
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                                                                                                     Query Match 79.5%; Score 260; DB 1; Length 50; Best Local Similarity 100,0%; Pred. No. 6.5e-27; Best Local Similarity 0; Mismatches 0; Indels No. Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      10 PSOCIYGVYYGNVTFHVPSNVPLKEVLWKKOKDKVAELENSEPRAFSSFK 59
                                                                                                                                                                                                               I PSOOIYGYVYGNYTPHVPSNVPLKEVLWKKQKDKVAELENSEFRAFSSFK 50
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                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/U649912

Sequence 7, Application US/U649912

GREMAL HOROMATON

APPLICAMT: BIOCHE, INC.

APPLICAMT: BIOCHE, INC.

APPLICAMT: MARKER SERVICE BROWNER

APPLICAMT: MARKER SERVICE BROWNER OF LIMBIOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE APPLICATION DAY:
APPLICATION NUMBER: US/08/459,512
CLASSEPCATION: 514
CLASSEPCATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIMESSFRANTING DAY
APPLICATION DAYNE:
APPLICATION NUMBER:
FILLING DATE: 12-MR-1992
APPLICATION NUMBER: US 07/567,971
FILLING DATE: 12-MR-1991
FILLING DATE: 12-MR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NOVERS: US 07/70,967
FILING DATE: US 07/70,967
FILING DATE: US 07/07-1991
ATTORNY AGENT INFORMATION:
NAME: HALEY, James F., J.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B151CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPERBUCE/DOCKET NUMBER: BI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEZ: 14-687
INFORMATION FOR SEQ ID NO: 2:
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875 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE PORM:
COMPUTER READABLE PORM:
WEDLUM TYPE: Flore.
COMPUTER READABLE PORM:
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LENGTH: 50 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
HYPOTHETICAL: NO
ANTI-CENT
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US-08-459-512-2
                                                ANTI-SENSE:
US-07-940-861-2
                                                                                                                                                                                                                                                                                            RESULT 2
US-08-459-512-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 PSQQIYGVVYGNVTFHVPSNVPLKEVLWKKQKDKVAELENSEFRAFSSFK 59
                                                                                                                                          MERRICONT WALKER, SETHER P.
APPLICANT WALKER, SETHER P.
APPLICANT WILLER, CHENT T.
APPLICANT WILLER, CHENT T.
APPLICANT WISSA, MASSACIATIO ANTIGES TO THE CONTRIBUTION WISSALS AND THE CONTRIBUTION WISSALS AND THE CONTRIBUTION WISSALS AND THE CONTRIBUTION WISSALS AND THE CONTRIBUTION TO 
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/667,971
FILICH DAFE: 12-MAR-1991
FILICH DAFE: 12-MAR-1991
FILICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DAFE: 07-007-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/459,657
02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMUTER REGIONALE FORM:
MEDIDH TYPE: Floppy disk
COMPUTER: INH PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4. US-08-460-132-2 US-08-460-132-2 US-08-460-132-3 Fatent No. 5258643 GENERAL INFORMATION:
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TELERAL (212)115-060
TELERAL (212)115-0673
INPOMENTOR TOR SED ID NO: 2:
SEDUREC CHARACTERISTICS:
LEMETH: 50 manno acids
TYPE: minno acid
STRANDEDESS: SINGLE
Sequence 2, Application US/08459657
Patent No. 5914111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 02-JUN
CLASSIFICATION: 424
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APPLICANT: BIOGEN, INC.

10 FSOQIYGVVYGNVTPHVPSNVPLKEVLWKKQKDKVAELENSEFRAFSSPK 59

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Sequence 6. Appl.1
Sequence 1. Appl.1
Sequence 1. Appl.1
Sequence 1. Appl.1
Sequence 1. Appl.1
Sequence 2. Appl.1
Sequence 3. Appl.1
Sequence 1. Appl.1
Sequence 1. Appl.1
Sequence 1. Appl.1
Sequence 2. Appl.1
Sequence 2. Appl.1
Sequence 3. Appl.1
Sequence 4. Appl.1
Sequence 5. Appl.1
Sequence 6. A
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SEQUENCE NO. 545-51

PRICE NO. 545-52

PRICE NO. 545-64

PRICE NO. 
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08-08-104-662-4
08-08-104-662-5
08-08-104-662-5
08-08-103-104-662-5
08-08-103-104-662-2
08-08-08-118-99-1
08-09-08-118-99-1
08-09-48-127-1
08-09-48-127-1
08-09-48-127-1
08-09-48-127-1
08-09-148-127-1
08-09-148-127-1
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PRIOR NUMBER: US 07/710,967
PRILING DATE: 07/710,967
ATTORNEY/APPLIT THROMATION:
NAME: RAIGE, James F., Jr.
RESERVENCE/DOCKET WINBER: 27,794
REPRENCE/DOCKET WINBER: BASICIPE
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
        Sequence 2 Appl.
Sequen
                                                                                                                                                                                                                                                                                           January 28, 2003, 08:58:45; Search time 14 Seconds
(*Mithout alignments)
128:200 Million cell updates/sec
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core greater than or equal to the accors of the result being printed,
and is derived by analysis of the cotal score distribution.
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1 LHCFGFISCFSQQIYGVVYG......DKVAELENSEFRAFSSFKNR 61
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-459-512-2
US-08-459-657-2
US-08-460-132-2
PCT-US92-02050-2
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US-08-328-152A-3
5185441-2
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US-07-709-091-1
US-07-709-091-4
US-07-709-091-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-730-465-2_COPY_20_80
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 61
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Match I
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No.
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Prilinked LEN-3 en
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Human CP13 surface
Human CD58 GP1 H
Human CD58 GP1 H
Human LFA-3 (CD58)
Human LFA-3 antige
Human LFA-3 antige
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tumen LFA-3 DID2RC
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tume
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fuman cell adhesio
Human cell adhesio
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Sheep LRA-3. Ovis
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Sheep LFA.3 protei
LFA.3 TM region de
Sheep LFA.3 delta
Sheep LFA.3 delta
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human diagno
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AAR05572
AAR20804
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AAY96127
AAU02436
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ABG18595
AAR60310
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AAR28369
AAR27163
AAY83136
AAB61160
AAU76228
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AAR34224
AAR60314
AAR28366
AAR28367
AAR60311
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AAY83134
AAB61158
AAU76226
AAR34222
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AAW04363
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/label-signal peptide
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29..222
/label=human LFA-3
1..28
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     03-JUN-1987;
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1094.5
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Protein
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AAP81507
     Lymphocyte functio
Sequence encoded b
Amino acid sequenc
Human LFA-3 protei
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Human LFA-3. Homo
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Human transmembran
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                                                                                                                                                                                                    January 28, 2003, 08:38:45; Search time 27:2194 Seconds (Without alignments) 1223:856 Million cell updates/sec
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1378-678-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-1378-0-137
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                             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAR27161
AAR64271
AAM04370
AAW3133
AAW31157
AAW31157
AAW34221
AAR34221
AAR34221
AAR28365
                                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 2000000000
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61 DKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLYV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD2-binding domain of lymphocyte function associated antigen-3 and DNA - for diagnosing and treating inflammation and auto:immune diseases, e.g. systemic inpus erythomatosus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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100.0%; Pred. No. 7.2e-118;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                Miller GT, Rosa MD, Wallner BP
                                                                                                                    92EP-0104320
                                                                                                                                                                              91US-0667971
                                                                                                                                                                                                           91US-0770967
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N-PSDB; AAQ28677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 AA;
                                                                                                                                                                              12-MAR-1991;
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                                                                                                                    12-MAR-1992;
                                                                                                                                                                                                           07-OCT-1991;
                                                          16-SEP-1992
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     RP503648-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDBDEYEMESPNITDTMKFFLYV 120
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                                                                                       DNA sequences encoding Lymphocyte Function Associated Antigen-3 which inhibits adhesion between T-lymphocytes and target cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Score 1326; DB 9; Length 250;
, Pred. No. 7.2e-118;
0; Mismatches 0; Indels 0;
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/note= "region deleted in M101
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Best Local Similarity 100.0%;
Matches 250; Conservative 0
                                                                                                                                                                              Disclosure: 1; 46pp; English.
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     WPI: 1988-368634/51.
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121 LESLPSPILTCALINGSIEVOCMIPEHYNSHRGLIMYSMDCPMEQCKRNSTSIYFKMEND 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the human 7 cell line which, eight offerful offerful sequence (met. 1502) detrived cell addesion protein PAPA. From Which a claimed protein comprision but man, IRA-3 since the first as damato-terminal activity, and colls (e.g. 7 colls) cultured in List presence, and professibly also in the presence of interlawdish's choose spanishes colly within this detach. No become improvement of the state of the presence of the pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell adhesion protein derived from LPA-3 - has immunosuppressant
effect and induces immunosuppressant cells when cultured in its
presence
                                                                                      Human; T cell; MOLT-4; cell adhesion; LFA-3; immunosuppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 7.2e-118;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishino T, Niwa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Pages 63-64; 83pp; Japanese.
                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                          /label- sig_peptide
                                                                                                                                                                                                                                                                                                                 29..250
/label- mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KANF ) KANEGAFÜCHI KAGAKU KOGYO KK.
                                                                                                                   cell line: immunosuppressant cell.
                            Human cell adhesion protein LFA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35,TP-0341959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95JP-0094060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamashita K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kakutani T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI: 1996-485732/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 DRKPDRTNSN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 DRKPDRTNSN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT38555
                                                                                                                                                                            lomo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-1995:
                                                                                                                                                                                                                                                                                                                                                                                                        HO9633217-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukuchi 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okazaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the full landupt form of human IRF1. This special contains a signal period and the ILF2. IN and ILF2. This special contains a signal period and the ILF2. IN and ILF2 contains a sequence were application cycle as the Victor Contain and the Nast the amen indeed the ILF2 contains the Nast the amenication was applicated by FGT. The aministral activity of Encologues of ILF2 contains the ILF2 contains th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDBYEMSSPHITDTMKFFLYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LESLPSPTLTCALTNGSIEVQCMIPEHYNSHRGLIMYSWDCPMEQCKRNSTSIYFKMEND 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LESLPSPTLTCALTNGSIEVOCMIPEHYNSHRGLIMYSWDCPMDOCKRNSTSIYFKMEND 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LPOKIQCTLSNPLFNTTSSIILFTCIPSSGHSRHRYALIPIPLAVITFCIVLYMNGILKC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WVASSDAGRALGVLSVVCLLHCFGFISCFSQQIYGVVFHVPSVVPFHVPSVVPLKEVLWKKQK 60
                       Mature form; human; ovine; LFA-3; antiviral agent; virus; infection; propagation cycle; HIV; PCR; primer; sheep; homologue; D1D2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVAGSDAGRALGVLSVVCLLHCFGFISCFSODIYGVVGNVTFHVDSNVPLKEVIMKKOK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An antiviral agent containing LFA-3 - useful on a virus with the same infection propagation cycle as HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1326; DB 15;
100.0%; Pred. No. 7.2e-118;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 15;
                                                                                                                                                                                                    /note= "Signal peptide"
29...250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 11-12; 18pp; Japanese
                                                                                                                                                                                                                                                                                    /note- "Mature LFA-3"
                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW04370 standard; Protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KANF ) KANEBUCHI KAGAKU KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           32JP-0318934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92JP-0318934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI: 1994-221795/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 DRKPDRTNSN 250
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es 250: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ70396
                                                                                                                                                                                                                                                                                                                                        JP06157334-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-NOV-1992;
                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seguence
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                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                              Peptide
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The presents againment is a specification relating to a switch of the presents againment is a specification relating to a switch of treases of relating prophylatas for a skin condition characterised by increased re-cell sectional and showness an action properties to the continuous and expension 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; antiallargic; vasotropic; skin condition;
Troch! a dheaton molecule CD2. lymphocyte function associated antigen-3;
IER-3; atopic dermatitis; cutameous T cell lymphome.
LESLPSPILICALINGSIEVOCMIPEHYNSHBGLIMYSWINCPMENCKRNSTSIYFKMEND 180
                                                                                                                                                                         181 LPONICOTISNEENTSSITTATCPSSGSSBBPALIFIELL
                                                               121 LESLPSPTLTCALTNGSIEVOCNIPEHYNSHRGLIMYSWDCPMEOCKRNSTSIYFKMEND 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prophytaxis or treatment of skin conditions such as dermatitis, inhibitor of T-cell adhesion molecule CDZ/Iymphocyte function-associated antigen-3
                                                                                                                                             CALICAMA LOTOTICA DE LA PROPERTA DEL PROPERTA DE LA PROPERTA DEL PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; transmembrane LFA-3; antipsoriatio; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Coiumn 25-28; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB61157 standard; Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0466465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0770969.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buman transmembrane LFA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wallner BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNMI ) UNIV MICHIGAN.
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                                                                                                                                                                                                                                                                                   241 DRKPDRTNSN 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-0CT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-1992:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-0CT-1992:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB61157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulation of this MyOAD interaction by admitistration of a CDD binding seast infinite CD2 signalling and T cell proliferation and activation and an are structured and not structured and structured and not structured and n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selective modulation of memory effector T lymphocytes by administration of a CD2 binding agent which inhibits the CD2/LFR-3 interaction useful for treating conditions such as inflammatory bowel diseases, psoriatio
                                                                                                                                                                                                                                                                                                                                                                                                                  LRA3; CD2; cell signalling; modulation; lymphocyte; T cell;
many effector T ymphocyte; pestakite architis;
rhemmicold architis; multiple sciences; acopt dermatitis;
rhemmicold architis; multiple sciences; acopt dermatitis;
ulcerative colitis; cutaneous T cell lymphoma; inhibition; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVAGSDAGRALGVLSVVCLLHCFGFISCFSQQIYGVVYGNVTFHVPSNVPLKEVLMKKQK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 67-68; 76pp; English,
                                                                                                                               AAY83133 standard: Protein: 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99W0-0820026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0098456
                                                                                                                                                                                                                                                                            24-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                  Human transmembrane LFA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 2000-282928/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB: AA293398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200012113-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-1999;
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This invention entailes to a moral ambout for presenting or treating stin
conditions characterised by increased "oil activation and abnormal
entition presentation in the densi and epidemia; The method comeries
inflation of washing-prophory a insention associated antique; and
inflation of the DZ/LAS, increased.

Inflation of the Inflation of Inflati
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22: Page 14-15: 32pp: English.
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92US-0862022.
92WO-US08755.
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                      05-DEC-2000; 2000US-0730465
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                                                                                   02-APR-1992;
06-CCT-1992;
06-JUN-1995;
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                                                                                   Gaps
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speldennia; still disorder; ypphoma, processis intopicals; lichen planus 
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                                                                                   Indels 0:
                                            Length 250;
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claimed in claim 22 of the specification"
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Interaction. This sequence is specifically
claimed in claim 22 of the specification"
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/note= "Peptide inhibitor of CD2/LFA3
interaction. This sequence is specifically
claimed in claim 22 of the specification"
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                                            DB 22;
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                                       100.0%; Score 1326; DB 22; 100.0%; Pred. No. 7.2e-118;
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                                                                                   0; Mismatches
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                                   Query Match
Best Local Similarity 100.0
Matches 250; Conservative
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121 LESLESPITCALINGSIEVQCHIPEHYNSHRGLIMYSWDCPMEDCKGNSTSIYFKMEND 180
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Pred. No. 4.6e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Improving tolerance of transplanted allo:graft or xenograft tissue - using LFA-3 or CD-2 binding protein esp. for humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                         AAR34221 standard: Protein: 250
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of antigen-linked skin conditions · using inhibitor of CD2-LFA-3 interactions for treating e.g. psoriasis UV damage, and
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Sequence encoded by a naturally occuring human transmembrane
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                                                                                                         CD2; LFA-3; transmembrane; phosphatidylinositol; T-cell.
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hes 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Pages 43-44; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           910S-0770969.
                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-US08755
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es 248: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cooper KD, Wallner BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-134148/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 HTKPDRTNSN 250
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                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                       06-OCT-1992;
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61 DKVABLENSPRAGSSPRINKYSDTVSGGCTTTRICTSSDDDBTWBSPRTDTWKFFVY 120
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                                                                               61 DKVAELENSEFRAFSSFRNRVYLDŢVSGSLŢIYNLŢSSDEDEYEMESPNIŢDŢMKFFLYV 120
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1 MVAGSDAGRALGVLSVVCLLHCFGFISSFSOO1YGVVYGNVTFHVPSNVPLKEVLMKKOK 60
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This con juty rates to plants members building imbunded the production of plants are produced to the plants are produced.
The contract of the plants are produced to the plants of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lymphocyte function-associated antigen (LFA-3) with
phosphatidylinositol (PI) linkage signaling sequence.
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                                                                                                                                                                                                                                                                                                                                             IRA-3-11ke protein; D2. region; IRA-3-delta D2; IRA-3; receptor; cell adhesion; immunogioulin; sperfamily; CD2; antique; D1; immunogioulin; representativ; CD2; antique; D1; immunogioulin; Like domain; transmentane region; Yr region; Trapion; C region; quivosiv; propolativiquinos; tol; gretain; disulphide bond; lymphocyte; function-associated; antique; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sheep LFA-3 protein and its derivs. - have high affinity for roells, useful for treating T-cell tumouts and leukaemia and also in diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohara T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                               AAR28365 standard; Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D2_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= TM_region
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91JP-0151792.
91JP-0154486.
91JP-0161377.
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                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label
                                                                                                                                                                                                                                                                      Human LFA-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 1992-408655/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1661-NOC-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-1991;
02-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1991;
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                                                                                                                                                                                      21-APR-1993
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Osakada

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Gaps

0 Length 240; Indels

Score 1250; DB 11; Pred. No. 1.2e-110; 1; Mismatches 0; 1; Mismatches

94.3%;

Conservative

Query Match Best Local Similarity Matches 236; Conserv

240 AA

Seguence

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Indels 0; Gaps

1 WVAGSDAGRALGVISVVCLLHCFGFISCFSQQIYGVYGNYFHYPSNYPLKEVLHKKQK 60

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Selective modulation of memory effector T lymphocytee by administration of a DD2 hindrag agent which inhibits the CD2/IRP3 interaction useful for treating conditions such as inflammatory bowel diseases, protabile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPA3, CD2, cell signalling; modulation: lymphocyte: T cell;
marry effector Tymphocyte; postation estrintis;
rhemmicol architis; multiple sciences; a topic dermetitis;
rhemmicol architis; antiple sciences; a topic dermetitis;
uiterstive colitis; custanous T cell lymphoms; inhibition; resement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recolation of LRAY/OZ Interection by administration of a CTS binding
sport inhibits CDS signaling and Teal; proliferation and activation ad-
and more particularly modulates the number and/or attribution of
among effector 7 lymphocytes. The method can be used for treating a
condition in a subject where the condition is characterized by memory
effector 7 lymphocytes playing a role in the psthopenesis of the
                                                                                                                                                                                                                                                                                                                                DKVAELENSEFRAFSSFKNRVYLOTVSGSLTIYNLTSSDEDEYEMBSPNTTDTMKFFLYV 120
                                                                                                                                                                                                                                                                                                                                                                                                 LESLPSPILTCALINGSIEVOCMIPEHYNSHRGLIMYSWDCPMEOCKRNSISYPKMEND 180
                                                                                                                                                                                                                                                                                                                                                                                                                        121 LESLESPTLTCALTNGSIEVOCMIPEHYNSHRGLIMYSWDCPMEGCKRNSTSIYFKMEND 180
                                                                                                                                                                                                                                                                                                    61 DKVAELENSEPRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLYV 120
                                                                                                                                                                                                                                                      1 MVAGSDAGRALGVLSVVCLLHCFGFISCFSQQIYGVVTGHVTFHVPSNVPLKEVLMKKQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPOKIGCTLSNPLFNTTSSILLTCIPSSGHSRHRYALIPIPLAVITCIVLYMNGM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPOKIQCTLSNPLFNTTSSILLTTCIPSSGHSRHRYALIPIPLAVITTCIVLYMNG1 237
                                                                                                                                                                                                       1 MVAGSDAGRALGVLSVVCLLHCFGFISCFSQQIYGVVYGNVTFHVPSNVPLKEVLWKKQK
contains the conformational requirements necessary for CD2/LFA-3
                                                                                                               Length 240;
                                                                                                                                                             Indels
                                                                                                               Score 1250; DB 13;
Pred. No. 1.2e-110;
                                                                                                                                                             ö
                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 69-70; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PI-linked human transmembrane LFA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY83134 standard; Protein; 240 AA
                                                                                                               94.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US20026
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                                                                                                                                                                  Conservative
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                                                                                                                                      Best Local Similarity
Matches 236: Conserv
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                                                                     240 AA;
                       complex formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ93399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40200012113-AZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degilavy D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis
                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY83134:
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy.
                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                             DKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLYV 120
                                                                                                                                                                                                            21 LESIPSPILTCALINGSIEVOCHIPEHYNSHBGLIMYSMDCPMBOCKRNSTSIYPKMBND 180
                                                                                                                                                                                                                                        121 LESLESPTITCALTNOSIEVOCNIPEHYNSHRGLINYSWDCPMEOCKRNSTSIYFKMEND 180
                       MVAGSDAGRALGVLSVVCLLHCFGFISCFSQQIYGVVYGNVTFHVPSNVPLKEVLWKKQK 60
                                         MAASSDAGRALGVISVCELLHCEGFISCFSOOTIGWTFHYPPINTER |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assistion element of PLT-REA's base prepared without provided at 
PLT-Linked surface polypeptide on Glo cells anving the kreaminal 89 
and actied on further IM-A'; The annin was generated by delettion 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mosphatidylinositol anchored lymphocyte associated antigen-3;
-lymphocyte accessory molecule; CD2 binding site; immunomodulator;
                                                                                                                                                                                                                                                                                                         181 LPOKIOCTLSNPLFNTTSSIILTTCIPSSGHSRHRYALIPIPLAVITTCIVLYMNGI 237
                                                                                                                                                                                                                                                                                                                                181 LPOKIQCTLSNPLFNPTSSILLTTCIPSSGHSRHRYALIPIPLAVITTCIVLYMNGM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD2-binding domain of lymphocyte function associated antigen-3 and DNA - for diagnosing and treating inflammation and auto: immune diseases, e.g. systemic lupus erythembtosus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PI-linked LFA-3 used to make PIM3 deletion mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "note- "deleted in mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 9-10; Fig 9; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR27162 standard; Protein; 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- PI-LFA-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- signal
29..240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller GT, Rosa MD, Wallner BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CMIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOJ ) BIOGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-1998
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The presents sequence is given in a specification relation to anticologic for treating or providing prophylatis for a faith condition characterised by increased real activation and abnormal matter motion characterised of providing the control of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LPQKIQCTLSNPLFNTTSSILLTTCIPSSGHSRHRYALIPIPLAVITTCIVLYMNGI 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.3%; Score 1250; DB 22;
99.6%; Pred. No. 1.2e-110;
1ye 1: Mismatches 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note- "Signal peptide"
                                                                                                                         Example 3; Column 29-32; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .ocation/Qualifiers
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READ 18-COMPANIEST: 3005-060927.

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MARCAD H.M.; Dellam G.M.; Dellam G.M.; Dellam G.M.; Dellam G.M.; Picklam G.M.; The Covolatt Structure of a human gamma G-immonglobulin. VII. Amino cold sequence of leavy-ofash cyanogen bromide fragments HI-HK-; Sischemistry 9:10[6:1370(1970).
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The nucleand M., Herstein B.J., Hood L.E.;
Wiche nucleatide sequence of a human immunoalobulin C gammal gene.";
Winchet Acids Res. 10:4071-4079(1982).
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BOUNDES 2299313 PubMed-688934;
Schuldt R. J. Jung J. M. Histombon M. Histombon M. Three-dhomsjoons Structure determination of entithodies. Primary Structure of Cerptailtized monoclonal manusoplandia. Immunoplantin 1991 NOL. 1.7;
proppe-891947 S. Physiol. Chem. 364713-747(1983).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDILHE-710405; PUDAGES PUDAGES DESUGAZ;
RULLEBANGSET U., Cunningham B.A., Bennett C., Konigsberg W.H.,
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Gall W.E., Boblama G. Roblama Gramunoglobulin. X.
"The Covalent structure of a human gamma G-immunoglobulin. X.
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21-JUL-1986 (Rel. 01, Last sequence update)
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Copyright (c) 1993 - 2003 Compugen Ltd.
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MUC_RABIT
                                                                                                                                                                            protein search, using sw model
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GC3_HUMAN
GC_RABIT
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GCB_RAT
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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IVC2_HETER

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121 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 GOPREPQVYTLPPSKDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTPPVLDS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
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SELLINGS OF 3-4 FORM LE-SERVEN
Ellisted A. HOOL LIE-SERVEN
LICKAGE and Sequence bemology of two human immunoglobulin gamma
heavy fahlin constant region general region general region general
Proc. Netl. Acad. Sci. U. S.A. '95:186-1988(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.4%; Score 1233; DB 1, Length 330;
100.0%; Pred. No. 2.3e-86;
ive 0; Mismatches 0; Indels
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Mommalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TextD-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36106 MW; 3770EE106C2FA33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GC2_BUMAN STANDARD; PRT; 326 AA. 001859; 21-70E-1986 (Rel. 01, Created) 15-70E-1986 (Rel. 01, Last sequence update) 16-70E-7901 (Rel. 40, Last semnotetion update)
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Matches 227: Conservative
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                                                                                                                                                                                                                                                                                                                  "Crystallorgeful: extrement and atomic podels of a human Per trament and its complex with frequent a of protein I A from Stephylococcusus acuses at 2.9 and 2.5 a. A resolution.", in Alondomistry 20.2516.22010;581.

**HOROGENISTY 20.2516.22010;5
                                                                                   288-272.
-- MESCELLANBOUS, KOL ALSO DIFFERS IN THE AMIDATION STATES OF
RESIDUES 199.2676272.
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/FIId=VAR_003887.
L -> M (IN GIM(NON-1) MARKER).
/FIId=VAR_003888.
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K -> R (IN GLM(3) MARKER).
/PTId=VAR_003886.
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                                                                                                                                                                                                                                                       X-AX CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; PubMed-7236608;
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Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
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Immunoglobulin domain; Immun
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
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PDB; 1PC2; 15-JUL-92.
Genew; HGNC:5525; IGHG1.
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120 VDKT-----HTCPPCPAPELLGGPSVFLFPPKPKPTLMISRIPEVICVVVDVSHEDPEV 173
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226 REMOVED POST-TRANSLATIONALIZ (FORDHARE).
60 S - A (IN HELDAN PROTEINS TIL 6 21E).
7FTIG4-WR 003899.
109 C - S (IN REF. 3).
35864 MR: 83108766876795 (EC64).
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ellison J.W., Buxbuum J.W., Mood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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Immunoglobulin domain; Immunoglobulin C region.
NOW TER 1 1
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                InterPro; IPR003306; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003609; Ig_like.
Pfam; PF0047; ig; 3.
SMRT; SW00410; IG_like; 1.
SMRT; SW00407; IGClike; 1.
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Genew; HGNC:5526; IGHG2.
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Floatuphide bridges of the heavy chain of human immunoglobulin G2.";
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                     SEGUENCE OF 88-115 FROM N.A.
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This strice your entry is copyright. It is produced through a collaboration between the Suisa institute of Bubinformatics and the Bubin outsation. The Bropose infortional treatment of the strice or settletistics on its medical and that its meant in the are no restrictions on its medical and that streamth those second these options of the strice allowes agreement (see http://www.isb-slb.ch/mnnounce/or send on earli to licenseelaboration).
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MEDIANCE 6.25(1955) Fubbed-e608565;
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MEDLINE-81021548; PubMed-6774747;
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InterPro: IPR0033507; Ig_cl.
InterPro: IPR0035607; Ig_llke.
Plam: PP0047; ig_llke.
SMART; SM00410; IG_llke; I.
SMART; SW00407; IG_llke; I.
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       This stress offer entry is copy. In the produced through a collaboration between the Sales institute of Bioinformatics and the Sens outsidence in Engineer the Sales institute of Marke are no institution of List manual and the Sales institutes and its modified and this streamt is not removed. Base by and for commercial entities an internal spreamed agreement (see http://www.isb-sib.ch/announce/or sens in small to themsetibribe.in)
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Plank J.R.L., Blattery S.B., de Vriess G.M., Milstein C.;
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Procedent region of a gamma 4 chain.";
Blochem J. 117:33-47(1970).
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22.-UU-1996 (Rel. 01. Last sequence update)
15.-UN-2002 (Rel. 01. Last sequence update)
15.-UN-2002 (Rel. 41. Last amucization update)
15.-UN-2002 (Rel. 41. Last amucization update)
15.-UN-2002 (Rel. 41. Last amucization update)
15.-UN-2002 (Rel. 01. Creation (Reavy chain disease protein) (HDC).
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InterPro: IPR003597; Ig_C1.
InterPro: IPR003600; Ig_like.
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SMART: SM00410; IG_like; 1.
SMART: SM00407; IGCl; 2.
PROSITE: PS00290; IG_MHC; 2.
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Genew; MGNC:5528; IGHG4.
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NEBPAT 59 73 PTRROLIDONE CARBOXYLIC ACID.	DISULFID 43 DISULFID 42 DISULFID 42 DISULFID 54 DISULFID 57 DISULFID 57 DISULFID 63 DISULFID 69 DISULFID 69	Considerty Con	227 227 K	SEQUENCE 290 AA; 32331 MM; Duery Match 60.7%; Sest Local Similarity 90.3%; Aatches 205; Conservative 13	Oy 121 DKTHTGPCRADELLGGSVILFPRKDTLAHSKYPENTCWOVSHEDPEVKRWIVD 180 Db 64 DTPPPGRGANBLLGGSVILFPRKRUTHAHSHTHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 181 OVDVHANKTREREGOINSTITWVSVLTVLAGDALAGEEKCKNSNERALPADIEKTISKAK 240 Db 124 OVDVHANKTREREGOINSTITWVSVLTVLAGDALAGEEKKRNSNERALPATEKTISKTR 183	Qy 241 GQPREPQPTTEPSENDEXTROWSSICTACKPPSD IANNESCORPREMATERIALS 300 Db 184 GQPREPQPTLPPSREEMTROWSITCACKREPPSDLAWERSSQPEMMYNTPPPHLIS 243	Qy 30 DASSETTARKITYDKSROGONYSESVARIAHETYOKSLESPEKK 347 Db 244 DASSETLYSKITYDKSROGONIPSKSVARIAHETYOKSLISPEKK 290	RESULT 5 CLANAIT PROJECT STANDAUD; PRIT; 313 AA. 1D 0.2.ANAIT PROJECT STANDAUD; PRIT; 313 AA. 1D 0.2.ANAIT PROJECT STANDAUD; PRIT; 313 AA. 1D 11.0.1.918 (PAI. 0) Late Standaud Prince Update Prince 11.0.1.918 (PAI. 0) Late Standaud Prince Princ	. 00 Z III = III III

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----HTCPPCPAPELLGGPSVFLFPPKPKDTLAISRTPEVTCVVVDVSHEDPEVKFN 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 SKTKGAPRMDDYTLPPSRDELSKSKUSVTCLIINFPADLHVBMASNRVPVSEKEYKNT
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKOGENER FROM N. N. NORG-GOT, POWDER-ENDING G.P., MATCLINER H.M., NORG C.P., NORG C.P., Raim D., Der-Balan G.P., Matcliner H.M., NORG P. N., Blatchene F.R., Structural analysis of the murine Igol constant region gene. ", PStructural analysis of the murine Igol constant region gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 346
                                                                                                                                                                                                                                                                                     Immunoalobulin C region; Glycoprotein.
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ENTERCHAIN (WITH A HEAVY CHAIN).
ENTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                    ENTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 N-LINKED (GLCNAC, . .).
308
36074 MW; 5D231B7164D1FBA9 CRC64;
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60.6%; Pred. No. 1.5e-60;
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Nus musculus (Mouse).
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01-AUG-1991 (Rel. 19, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                               HSSP, P01842; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
                                                                                                                       Interpro: IPR003600; IQ_11ke.
Pram, PR00047; 42; 2
SWART; SW004.07; IG_11ke: 1
SWART; SW004.07; IG_11ke: 1
SWART; SW004.07; IG_11ke: 1
IRRNORING; IG_11ke: 1
IRRNORING; IG_11ke: 1
IRRNORING; IG_11ke: 1
IRRNORING; IG_11ke: 1
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79
105
110
202
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      PTR: A02151: G2GP
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DI SULFID
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"Interchia disulfation of guinea pig gamma-2-immunoglobulin.";
Bacchemistry 10.26-31(1971)
--- HISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
                                                                                                    103 PTCPPPELLGGPSVPIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT 162
                                                                                                                                                                                      187 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 246
                                                                                                                                                                                                                                                                                                                                                    223 KVYTWGPPREELSSRSVSLTCMINGFYPSDISVEWERNGKARDNYKTTPAVLDSDGSYFL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There K.J.; Cabta J.J.;
Structure of heavy chain from strain 13 quines pig-
leminoglobulin-G(2). II. Amino anid sequence of the carboxyl-terminal
minographor cyanogem from transfe fragments.';
strochmatery lot-17(17)1,
51 RTPPSVROSSGLXSLS---SVVSVTSSSOPVTCNVAHPATNTK-----VDKTVAPSTCSK 102
                                                               PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYUDGVEVHN 186
                                                                                                                                                                                                                                                      163 ARPPLREOOFNSTIRVOSTLPITHODWLRGKEFKCKVHNKALPAPIFKTISKARGODIEP 222
                                                                                                                                                                                                                                                                                                                     QVYTLPPSRDELTKNOVSLTCLVKGPYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFL 306
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'Structure of heavy chain from strain 13 guinea pig
immunosiobulin-G(2). S. Amino acid sequence of the region around the
Blochemstery lois18-25(1971).
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TRIGHT-5050675. PubMed-4(23665.
TROORD D.E., Cebra J.J.,
TROORD D.E.,
TROORD D.
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Trischmann F.W., Cebra J.J.;
Primsty Structure of the GHB Nemology region from guines pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 gamma-2 chain C region.
Cavia porcellus (guinea pig).
Rekaryota Metzaca, Chordata; Creniata; Vertebrata; Euteleostomi; Mammalia; Eutherias, Rodentia; Rod
                                                                                                                                                                                                                                                                                                                                                                                                                                             307 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSFGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 YNKLSVPTSEWORGDVFTCSVMHEALHNHYTOKSISRSPGK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1975) to the PIR data bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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MEDLINE=71058486; PubMed=5538616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 4-68.
MEDLINE-71058471; PubMed-5538606;
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SEQUENCE OF 227-311
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This BRISS FOUR marks is opergitable. It is produced through a collaboration between the Suss institute of Bioinformatics and the EMBG collation. The Engagement institution "There are no restrictions on 11st modified and this statement is not removed. Broad production and the engineering of the engagement of the commercial modified and this statement is not removed. Broad product commercial entities regulate a license agreement (see http://www.isb-sib.ch/announce/or send an easil to licensestiab-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 HTAQTOPREDOYNSTPRVVSALPIQHODWASGKEFKCKVNNKALPSPIEKTISKPKGLVR 230
                                                                                                                                                                                                                                                                                                                                                                                         125 TCPPCPAPELLGGPSVPLEPPXPXDIAISRTPRVTCVVVDVSHRDPBVEVMFNMYVDGVRV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 HNAKTKPREDZINSTYRUZSUIJULHODBIJNSKEYKCKUSNKALPAPIEKTISKAKGOPR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 EPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TOXID=10090;
                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 128-398 FROM N.A.
REDLIND-80404183; PubMed-6314258;
Komarowy M., Clayton L., Rogers J., Robertson S., Kettman J.,
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                          Score 838; DB 1; Length 333;
Pred. No. 1.9e-56;
                                                                                                                                                                                                                                                                                                                 42; Indels
                                                                                                                                                                          36497 MW; 55F8B64D48D460A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 PLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSpGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-057-1986 (Rel. 02, Created)
01-A0G-1991 (Rel. 19, last sequence update)
15-JUL-1999 (Rel. 18, last amtocation update)
15-ADAMES - Tobain C region, membrane-bound form.
Nas musculus (Mouse).
                                                                                                                                                                                                                                                                                                                 33; Mismatches
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Nucleic Acids Res. 11:6775-6785(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT:
                                                                                                                                                                                                                                                 45.28;
                                                                                                                                                                                                                                                                                     66.48.
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                                                                                                                                                                                                                                                                                                                 Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
109
112
115
147
253
333 AA;
                                                                                                                                                                                                                                                                                     Local Similarity
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DISULFID
DISULFID
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                                                                                                                                                                          SECUENCE
                                                                                                                                                                                                                                                 Query Match
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EEEEES
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OFED-199 (Rel. 17, Last sequence undate)
19 paines 20 Abil (Caretard)
19 paines 20 Abil (Caretard)
19 paines 20 Abil (Caretard)
19 paines (Rel.)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brussgemann h.
Prussgemann h.
Gene 74:473-482(1968).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 PP---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 REPQVYTLPPSRDELTKNQVSL/CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3,
                                                                                                                                                                                                                                                                                                                                              PROSITE: PS00290; IG_MHC; 1.
Immunoqiobuin domain: Immunoqiobuin C region; Glycoprotein;
Transmembrane: Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.6%, Score 845.5; DB 1; Length 329;
67.0%, Pred, No. 5.1e-57;
Live 34; Mismatches 37; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 113 HINGE.
114 223 CH2.
224 37 CH3.
329 AA: 36228 MM; F45827174182BADG CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 YPLYSKLTVDTDSWLQGELFTCSVVHBALHNHTOKNLSRSPGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS00290; IQ_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CH1.
HINGE.
CH2.
                            -; NOT_ANNOTATED_CDS
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MEDLINE-89232738; PubMed-3149946;
                                                                                                   HISSP: P01857; IFO.
InterPro: IPR0013005; Ig_MEC.
InterPro: IPR0013005; Ig_Cl.
InterPro: IRR0013600; Ig_Like.
Flam: PP000047; Ig_ 3.
SHART; SM00400; IG_Like; I.
SHART; SM00407; IGCL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR003006; Ig_MHC.
Interpro; IPR003057; Ig_C1.
Interpro; IPR003609; Ig_L1ke.
Pfam; PP00047; ig; 3.
SWART; SW00410; IG_Like; 1.
SWART; SW00407; IG_Like; 1.
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HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                PIR, B02156; G3MSC
HSSP; P01857; 1FC1
                                   .100451:
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DOMAIN
DOMAIN
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P20761:
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92 IYNLTSSDEDEYEMESPNITDTMKFELYDKIHTCPPC-PA-----PELLGG--- 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 PCICTGSEVSSVPIFPPRPKPKDVLTITLTPRVTCVVVDISQDDPEVHFSWFVDDVEVHTAQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIRKTISKAKGQPREPQV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signere or 75-24 FORM A. A. (PELOMA PORTER MORE JILC).

WINDLINE-GROZZÓS, PUBMEG-GFGSTS.

ORDEL N. T. SEMBARI S. T. SEMBARI N. SEMBORI T. SEMBARI A.,

WHON I. SEMBARI S. T. PREMILIE B. N. LEGGE C. T. REDIO T. SEMBARI A.

ELONG I. D. BERCHELL B. N. LEGGE C. T. REDIO T. SEMBARI A.

ELONG I. D. BERCHELL B. N. LEGGE C. T. REDIO T. SEMBARI A. SEMBARI S. T. SEMBARI T. S. M. LEGGE C. T. REDIO T. SEMBARI T. S. M. LEGGE C. T. REDIO T. SEMBARI T. S. M. LEGGE C. T. REDIO T. SEMBARI T. S. M. S. M. SEMBARI T. S. M. S. M
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SEQUENCE OF 770-322 PROM N.A. (MYELOMA PROTEIN MOPC 21).
ROGERS T. Clarke P., Salser W.;
Rogers T. Clarke P., Salser W.;
Passuence analysis of cloned cDNA encoding part of an immunoglobulin haavy chain. 1, yel
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Memmaliari Eniberia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NGELTRO-10090;
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                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
013BaB45EF49B9DA CRC64;
                                                                                                                                                                                                                                          36;
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"Evolution of immunoglobulin subclasses. Primary structure of murine myelome gamma! chain.";

anution myelome gamma! chain.";

J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                       Length 326;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                          45: Mismatches 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 KLTVDKSRWQQGNVPSCSVMHEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 KLAVVKEKWQQGNTFTCSVLHBGLHNHHTEKSLSHSPGK 326
                                                                                                                                                                       44.1%; Score 819; DB 1;
54.8%; Pred. No. 5.1e-55;
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POTERBOAD
21-70U-1986 (Rel. Ql. Created)
21-70U-1986 (Rel. Ql. Last Aequence update)
N-MY-2000 (Rel. 39, Last annotation update)
Iggamma-1 chain C region.
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MEDLINE-78242288; PubMed=98524;
      140 200
246 304
176 176
326 AA: 35946 MW; (
                                                                                                                                                                                                                Best Local Similarity 54.8%
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD:
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DISULFID
DISULFID
CARBOHYD
                                                                                                           SEQUENCE
                                                                                                                                                                              Query Match
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GC1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 VHTANTOPREACYNSTPRVVSALPIOHODHWRGKEFKCKVNNKALPAPIERTISKFKGRA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 QTPQVYTIPPPREQMSKKVSLTCLVTWPFSEAISVEWERNGELEQDYKNTPPILDSDGT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-785-1391 (et. 17. Cerebed)
13-701-1391 (et. 17. Cerebed)
13-701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Indels 3;
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Immunopidobilin domain; immunopidobilin C region; Glycoprotein.

Immunopidobilin domain; Immunopidobilin C region; Glycoprotein.

Immunopidobilin domain; Glycoprotein.

Immunopidobilin domain; Glycoprotein.

Immunopidobilin domain; Glycoprotein.

Immunopidobilin domain; Glycoprotein.
                                 propriet profession 16_MHC; 1.
PROSTIE: PRODEOUS 16_MHC; 1.
Immunoglobulin Gomelair Immunoglobulin Gomelair Immunoglobulin Gomelair Emmelairene; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.0%; Score 814.5; DB 1; Length 398; 66.7%; Pred. No. 4.4e-56;
                                                                                                                                                                                                                                                                                                                                               398 CYTOPLASMIC (POTENTIAL).

332 E -> G (IN REF. 2).

342 E -> Q (IN REF. 2).

368 P -> F (IN REF. 2).

43929 MM; CF7F264B50AA1B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTOKSLSLSP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 YPLYSKLTVDTDSØLGGEIFTCSVVHBALHUHHTGKNLSRSP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Mismatches
                                                                                                                                                                                                                                                                                                                    DOTENT AL
                                                                                                                                                                                                                HINGE.
CH2.
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MEDLINE-89232738; PubMed-3149946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00290; IG MHC: 1.
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Matches 148; Conservative
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SMART; SM00407; IGc1; 2.
      SMART; SM00407; IGC1; 2.
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342 3
388 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 CPAPELLGGPSVFLFPPKPFLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 TEPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 248
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Frate disupplied bridges of a mouse lamunoglobulin G1 protein.*;

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BMBL, V00795; CAA24176.1; --
PIR, A02199; GAA24176.1; --
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10-WAY-2000 (ed.) 19. Late 'squaren update)
10-WAY-2000 (ed.) 19. Late 'squaren specials' post of the same of the same
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MEDLINE-82115295; PubMed-6799207;
Rogers J., Chot B., Souza L., Carter C., Word C.J., Kuehl M.
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immunoglobulin gamma chains.";
Gell 26:19-27(1981).
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21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tall-1986 (Rel. 01. Lates sequence update)
21-70L-1986 (Rel. 01. Lates sequence update)
81-70L-1986 (Rel. 01. L
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Nucleic Acids Res. 8:3143-3155(1980).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
                                                                               Pfam, PF00047; 19: 2.
SMART, SM00410; IG.11ke; 1.
SMART; SM00407; IGC1; 2.
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329 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 LDIVSGSLTIYNLTSSDEDEYEMESPNITDIMKFFL-----YVDKTHT-----CPP-- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LYTLSSSVTV-----PSSPRPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 CPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 CTVPEV---SSVFIFPPKFKDVLTITLTPKVTCVVVDISKODPEVQFSWPVDDVEVHTAG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 TKPREBOYNSTYRVUSULTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOV 248
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13-501/291 (Re. 17. Last sequence update)
13-501/291 (Re. 13. Last sequence update)
13-501/291 (Re. 13. Last sequence update)
13-501/291 (Re. 13. Re. 10. Last sequence update)
13-501/291 (Re. 13. Re. 10. Last sequence update)
13-501/291 (Re. 13. Re. 10. Last sequence update)
13-501/291 (Re. 13. Re. 13. 
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PRUGITING-REBIGGO31 PubMed-4312722; P. Waldmann H., Calabi F.;

PRUGIGGOBERMIN M. DeBRASTIC Gelffee, P. Waldmann H., Calabi F.;

Sequence of a reat immunosjobniin gamma 2 cb heavy chain constant
region CNMH: eteraise (bebology to mouse gamma 3.7;

Immunol. 31 Faminol. 18:317-319(1888)
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Pred. No. 1.7e-54;
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This SMSS port entry is opergight. It is produce through a collectuous between the SMSs institute of inclinionatius and the BBM contestion the European bonformattics institute. There are no restrictions on its mass of the operation of the statement of the state
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Mammalla: Eutherla: Rodentla: Sciuroquathi: Muridae: Musinae: Mus
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305 FLYSKLTVDKSRWODGNVFSCSVNHEALHNHYTOKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                         21-201-1986 (Rel. 01, Created)
Andreis91 (Rel. 19, Jast sequence update)
15-201-1999 (Rel. 18, Last sequence update)
15-301-1999 (Rel. 18, Last sequence update)
15-301-1999 (Rel. 18)
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54.6%; Pred. No. 5.8e-54;
                                                                                                                                                                                                                                                                                                        399 AA
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InterPro; IPR003597; ig_cl.
InterPro; IPR003600; ig_like.
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MGD; MGI:96443; Igh-1.
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                                                                       DAIDAR - DAZEJONY C., MOSCHAMPS C., Rougeon F.; Rougeon F.; Moschamps C., Rougeon F.; And gamma 2b chain genes suggests from the tennos can be exchanged between genes in a multipanic
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37; Mismatches 60
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100.0%; Pred. No. 1e-99;
Live 0; Mismatches 0; Indels
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Signemer rose Na. A. Medical processor rose Natural Resource C., Albora W., Richards C., Albora M., Rollands W., Richards C., Albora M., Albora W., Radrands C., Albora M., Rollands W., Radrands C., Albora M., Rollands W., Radrands C., Albora M., Rollands W., Radrands C., Albora W., Radrands C., Carlon C., Albora W., Radrands C., Carlon C., Radra C., Radr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 NAKTKPREBQFNSTYRVSVLTTULHIHIHIHIHIHIHIH H: HIHIHIHIHIHIHIHIH
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BCQ25985; AA425985.1; ".
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 473 AA; 51986 MM; R29920B0369F5 CRC64;
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01-DEC-2001 (TEMBLEGI. 19, Created)
01-DEC-2001 (TEMBLEGI. 19, Last asquence update)
01-DEC-2001 (TEMBLEGI. 11, Last andocation update)
Immunogobolin gamma. Theavy Chain constant region
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Best Local Similarity
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TISSUE-KIDNEY;
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BEALWRA-137746; Prob N.A.

Property (17 Head of 17 Head o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 300
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eurharia; Primates; Catarrinis; Nominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ë
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100.0%; Pred. No. 1.7e-99;
ive 0; Mismatches 0; Indels C
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                                               425 DGSFFLYSKLIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
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01-DEC-2001 (TFDMELrel. 19, Last sequence update)
01-DEC-2001 (TFDMELrel. 19, Last semunocation update
02-05 (TFDMELRel. 10, Last semunocation update
03-05 (TFDMELRel. 10)
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QBTC63;
01-JUN-2402 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                               DRT:
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83 LDTVSGSLFIYNLTSSDEDEFEMESPNITDTMKPPLYVDKTHTCPp--CPAPELLGGPSV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 FLFPPKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYVDGVEVHNAKTKPREEQINSTY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 PIPPPKPKDVLTITLTPKVTCVVVDISKDDPEVQPSWFVDDVEVHTAQTQPREEQFNSTF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREDOVYLLPPSRDELIK 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 DKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYPIYSKLNVQKSNWEAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
WCBL_Taxilo10090,
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                                                                                                                                                                                                                                                                                                                                              Query Match

44.7%; Score 830.5; DB 11; Length 463;
Best Local Saillarity 56.6%; Prod. No. 1.9s-64.

Matches 151; Conservative 49; Mismarches 62; Indels 5;
                                 Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOB455, AMB03455.1; ...
HSSP; P01842; FPRB.
                                                                                                                                                                                                                                                                        SMART: SMOO410: IG_11ke; 1.
PROSITE: PSO0290: IG_MIC. UNKNOWN_1.
SROURICE 63 AA; 51007 WM: BAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNIN-2002 (TrEMBLrel. 21, Last annotation update)
Gammal heavy chain of Mab7 (Fragment).
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                                                                                        MGD; MGI:96446; Igh-4.
InterPro; IPR00359; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Iq_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEam, PF00047; 19: 4.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 2.
                                                                                                                                                                                                                                       IGC1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                      ig; 4.
                                                                                                                                                                                                                                   SMART; SMO0407; IGC1;
SMART; SMO0406; IGC1;
SMART; SMO0410; IG_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
SEQUENCE PROM N.A.
                                                                                                                                                                                                                        SM00409;
                                                                                                                                                                                                  Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                        SMART:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGH-4
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                                 114 CPKCPAPELLGGPSVPIPPPNPKDTLMITRIPEWTCVVDVSQENPDVFNWYMDGVEVR 173
                                                                                                          249 CKPCICTVPEV---SSVFIFPFRKDVLIIIITFRVVTCVVVDISKDDPEVQFSWFVDDVE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 CPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 185
                                                                                    186 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPRE 245
                                                                                                                                                             246 POVYTLPPSRDELTKNOVSLICLVKGPYPSDIAVENESNGOP--ENNYKTTPPVIDSDGS 303
                                                                                                                                                                                   44.8%; Score 831.5; DB 11; Length 469;
63.8%; Pred, No. 1.6e-64;
tive 41; Mismatches 35; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 CPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridee; Mus. Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stronderg R.:
Submitted (MMK-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BCD44(05. AMK24405.1; -
Hypthetical Protein: 5347937155D05457 CRC64;
                                                                                                                                                                                                                                   304 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                     294 FPLYSKLSVDRNRWQQCTTFTCGVMHEALHNHYTQKNVSKNDGK 337
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01-JUN-2002 (TERBELTEL) 21, Last sequence update)
01-JUN-2002 (TERBELTEL) 21, Last annotation update)
Hypothetical 22 or Kba protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last Sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                    469 AA
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01-UNN-2001 (TERMILE1. 17, Created)
01-UNN-2001 (TERMILE1. 17, Last sequol-UNN-2002 (TERMILE1. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    datches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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126 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNHYVDGVEVH 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTI------KPC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 PPCKCPAPNLLGGPSVPIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVJSWFVNVEV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.7%; Score 811; DB 11; Length 473;
64.0%; Pred, No. 1e-62;
ive 38; Mismatches 42; Indels C
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Intereor IRROGADOS, 19 JMC.
Plane PRODORY 194, 194.
SMATS SMOODY 154, 152, 2
SMATS SMOODY 156, 12
SMATS SMOODY 156, 13
SMATS SMOOTH 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
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Matches 142; Conservative
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Matches 155; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 LDTVSGSLTIYNLISSDBDEYEMESPNITDTMKFFLVVDKTHTCPP--CPAPELLGGPSV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEV---SSV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 PLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 RVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSFWOOG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKVSLFCMITDFFPEDITVENQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAG 410
                                                                                                                                                                                                                                                                                                                                                                                                    5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Punctional annotation of a full-length mouse cDNA collection."; where 409:685-696(2001). 
EMBL: AROP318; BAR25349.1; -.
                                                                                                                                                                                                                                                                                        44.5%; Score 826.5; DB 11; Length 437;
56.2%; Pred. No. 4e-64;
                                                                                                                                                                                                                                                                                                                                                                                                    62: Indels
                                                                                                                                                                                       437 AA; 48142 NW; 5C3A7BB3EE7D697C CRC64;
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10.-20N-2001 (TERBirel. 17, Last sequence update)
10.-00C-7001 (TERBIREL. 19, Last sequence update)
10.00C-02NH FORTER. 19.
108.1910960098HR.
                                                                                                                                                                                                                                                                                                                                                                                                    Matches 150: Conservative 50: Mismatches
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                     PROSITE; PS00290; IG MHC; UNKNOWN 1
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MEDLINE-21085660; PubMed-11217851;
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_11ke.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTI-----NPCPP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 -----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 PREPQVYTLPPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKITPPVLDSDG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29; Gaps
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10-DECOSOI (TERBELCEI. 19, Created)
01-DECOSOI (TERBELCEI. 19, Cata sequence update)
01-DECOSOI (TERBELCEI. 19, Last sequence update)
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42.34; Score 784.5; DB 11; Length 474;
Best Local Similarity 53.04; Pred. No. 21e-60;
Matches 151; Conservative 43; Masketches 62; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vuery Match (2.3%; Score 784.5; DB 11; Length 473; Best Local Similarity 53.0%; Pred. No. 2.1e-60; Matches 151; Conservative 43; Mismatches 67; ....
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Special Control of the DeblyContain Arithmetic Control of the DeblyContain Arithmetic Control of the Control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 473 As; 51946 MW; CF625F008932AF12 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 LDTVSGSLTIYNLT-----SDEDEYEMESPHITDTMKFFLYVDKTHTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 PP.--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNWYVDGVEV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 BPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 304
                                               185 HNAKTKPREEDYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                       Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoai;
Mamaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Nurinae; Mus.
NCBL_TAXID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 43.5%; Score 807.5; DB 11; Length 473; Local Similarity 54.8%; Pred. No. 2e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    305 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
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01-JUN-2001 (T-EMBLrel. 17, Last Sequence update)
01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
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                                                                                                                            Homo sapiens (Human).
Makaryota, Necaza, Chordata, Craniata, Vertebrata; Euteleostoml;
Nammalia; Euthertaza, Primates; Catarrhini; Howinidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Enkaryota: Wetazoa: Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Caterrhini; Hominidae; Homo.
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KILDA LAST986.16; PubMed-7345392;
KILDA N.C. HILI V., Olsen I., Porter S.R.;
KILDA D.S. a novel in vivo lasform of lymphocyte function-
associated antigen 3.4:
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Pred, No. 1.2e-30;
www.netches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                    SOUTENCE FROM N.A.
RANLORD T.:.
SOBELLOG T.:.
SOBELLOG (FEB-1994) to the EMBL/GenBank/DDBJ databases
EMBL, DSBS66; BANA09422.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            79BEF0A4EEB4E59B CRC64;
014748;
01.80V-1996 (TrEMBLrel. 01, Created)
01.80V-1996 (TrEMBLrel. 01, Last sequence update)
01.80Z-2001 (TreMBLrel. 19, Last annotation update)
LEAP-3(delta D2) (Freqment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 SSDEDEYEMESPWITDTMKFFLYV -- DKTHTCPPCPAP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SSDEDEYEMESPNITDTMKFFLYVLGHSRHRYALIPIP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.6%; Score 476; DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SLTIYNLTSSDEDEYEMESPNITDTMKFFLYV 92
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Job time : 75.2362 secs
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SMART; SM00409; IG; 1.
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Best Local Similarity
                                                                                                                                                                                                            NCBI_TaxID-9606;
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                                                      99 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTI-----NPCPP 249
                                                                                                        29 -----CPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNWYVDGV 182
                                                                                                                                 310 EVHTAGTOTOTHERDYNSTIRVVSALPTOHODAMSGGERFCKVNNKDLPSPIERTISKIKGI. 359
                                                                                                                                                                                                                                                                                                           243 PREPOVYTEPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDG 302
                                                                                                                                                                                                                                                                                                                                    61 DKVAELENSEFRAPSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DKVARLENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMBSPNITDTMKFFLYV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DKTHTCPPCPAPELLGGPSVELFPPKPKDTLMISRTPEVTCVVVDV--SHEDPEVKFNWY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 LES-----LPSPTL-----TCALTNGSIEVOCMIPEYYNSHRG-LIMYSW- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 VDGVEVHNAKTKPREE-QYNSTYRVUSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 LDTVSGSLTIYNLT------SSDEDEYEMESPNITDTMKFFLYVDKTHTCPP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVAGSDAGRALGVLSVVCLEHCFGFISCFSQQIYGVVFFHVPSNVPEKEVLWKKQK 60
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                                                                                                                                                                                                            183 EVHNAKTK PREBOYNSTYRVVSVLTVLHODWILNGK EYKCK VSNKALPAPIEKTISKAKGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eskaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01.0NN-2001 (TFEMBLEAL. 17, Created)
01.0NN-2001 (TFEMBLEAL. 17, Last sequence update)
01.0NN-2001 (TFEMBLEAL. 19, Last sequence update)
01.0NEC-2001 (TFEMBLEAL. 19, Last annotation update)
Similar to CDS8 antigen, (lymphocyte function-associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.1%; Score 632.5; DB 4; Length 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 SIILTTCIPSSGHSRHR--YALIP----IPLAVITTCIVLYMNGMY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-BRAIN;
Strausberg (APR-2001) to the EMBL/GenBank/DDBJ databases;
SUBAILted (APR-2001) to the EMBL/GenBank/DDBJ databases;
HSRB, P19255; LCC2.
                                                                                                                                                                                                                                                                                                                                                                                                          103 SFFLYSKL/TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SMO0409; IG; I.
SEQUENCE 240 AA; 27044 MW; 431E44EFEDDF80B2 CRC64;
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